

Thu Oct 14 09:29:46 2004

us-10-021-002-2.ra1

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OM protein - protein search, using sw model

Run on: October 13, 2004, 18:08:19 : Search time 21 Seconds
(without alignments)
997.928 Million cell updates/sec

Title: US-10-021-002-2

Perfect score: 1659

Sequence: 1 MVELMPFLILLPFLLYMA.....RNETIARLMDVITCWSAQ 316

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1659	100.0	316 1 US-08-464-400-2	Sequence 2, Appli
2	1659	100.0	316 3 US-08-875-273A-2	Sequence 2, Appli
3	1659	100.0	316 3 US-09-123-346-2	Sequence 2, Appli
4	1659	100.0	316 5 PCT-US93-0187A-2	Sequence 2, Appli
5	1577	95.1	318 3 US-09-439-313-339	Sequence 338, App
6	1577	95.1	318 3 US-09-352-616A-339	Sequence 338, App
7	1577	95.1	318 4 US-09-636-215-339	Sequence 339, App
8	1577	95.1	318 4 US-09-685-166A-339	Sequence 339, App
9	1577	95.1	318 4 US-09-679-426-339	Sequence 339, App
10	512.5	30.9	309 4 US-09-270-767-4172A	Sequence 4172A, A
11	494.5	29.8	323 2 US-08-580-545B-2	Sequence 2, Appli
12	494.5	29.8	323 3 US-09-262-655A-2	Sequence 2, Appli
13	474	28.6	330 4 US-09-489-847-162	Sequence 162, App
14	466.5	28.1	320 2 US-08-530-165-7	Sequence 7, Appli
15	454	27.4	330 4 US-09-489-847-330	Sequence 330, App
16	443	26.7	380 4 US-09-252-991A-32854	Sequence 32854, A
17	427.5	25.8	407 4 US-09-270-767-43967	Sequence 43967, A
18	381.5	23.0	274 4 US-09-328-352-8213	Sequence 8213, Ap
19	359.5	21.7	287 2 US-08-901-306-2	Sequence 2, Appli
20	354.5	21.4	287 3 US-09-180-271-2	Sequence 2, Appli
21	275.5	16.6	336 4 US-09-248-796A-15559	Sequence 15559, A
22	262.5	15.8	354 4 US-09-248-796A-16822	Sequence 16822, A
23	260	15.7	401 4 US-09-248-796A-16145	Sequence 16145, A
24	254	15.3	503 4 US-09-248-796A-15340	Sequence 15340, A
25	254	15.3	507 4 US-09-792-024-109	Sequence 109, App
26	238	14.3	148 3 US-09-724-864-41	Sequence 41, Appl
27	229	13.8	203 4 US-09-634-955B-26	Sequence 26, Appl

28	227	13.7	203 4 US-09-634-955B-17	Sequence 17, Appl
29	224.5	13.5	107 4 US-09-270-767-33908	Sequence 33908, A
30	224.5	13.5	107 4 US-09-270-767-49125	Sequence 49125, A
31	222	13.4	203 4 US-09-634-955B-20	Sequence 20, Appl
32	219	13.2	294 4 US-09-328-352-4992	Sequence 4992, Ap
33	215.5	13.0	238 4 US-08-586-664-1	Sequence 1, Appli
34	215.5	13.0	248 3 US-09-385-028-11	Sequence 11, Appl
35	215.5	13.0	248 4 US-09-726-614-11	Sequence 11, Appl
36	215.5	13.0	248 4 US-09-385-040-11	Sequence 11, Appl
37	209	12.6	267 4 US-09-252-991A-32380	Sequence 32380, A
38	209	12.6	339 4 US-09-148-545-248	Sequence 248, App
39	206.5	12.4	632 4 US-09-328-352-6485	Sequence 23096, A
40	203.5	12.3	318 4 US-09-148-545-192	Sequence 192, App
41	203.5	12.3	318 4 US-09-148-545-192	Sequence 192, App
42	200	12.1	300 4 US-09-907-794A-159	Sequence 40, App
43	200	12.1	300 4 US-09-866-028-37	Sequence 37, Appl
44	200	12.1	300 4 US-09-905-125A-159	Sequence 159, App
45	200	12.1	300 4 US-09-902-775A-159	Sequence 159, App

ALIGNMENTS

RESULT 1
US-08-464-400-2
Sequence 2, Application US/08464400
Patent No. 5786204
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Prostatic Specific Reductase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,400
FILING DATE: Concurrently
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-464-400-2

Query Match 100.0%; Score 1659; DB 1; Length 316;
Best local Similarity 100.0%; Pred. No. 1.1e-186; Index 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVELMPFLILLPFLLYMAPOIRKMLSGVCTSTVQLPGKVVVVGANTGIGKETAKE 60

Db 1 MVELMPFLLLLLPFLLYAAAPQIRKMLSSGVCTSTVQLPGKVVVVVTGANTGIGKETAKE 60
QY 61 LAORGARVYLACRDVEKSELVAKEIOTTGNOQVVRKLDJSDTKSIPAMAKGFAEKH 120
Db 61 LAORGARVYLACRDVEKSELVAKEIOTTGNOQVVRKLDJSDTKSIPAMAKGFAEKH 120
QY 121 LHWINNAGVMMCPYSKTADGFEHMIQVNHJGHFLLTHLLEKLESAPSRIVNSSLAH 180
Db 121 LHWINNAGVMMCPYSKTADGFEHMIQVNHJGHFLLTHLLEKLESAPSRIVNSSLAH 180
QY 181 HLGRIHFHNLQGEKRYNAGLAYCHSKLANILFTQELARLKGSGVTTYVHPGTVOSELY 240
Db 181 HLGRIHFHNLQGEKRYNAGLAYCHSKLANILFTQELARLKGSGVTTYVHPGTVOSELY 240
QY 241 RHSSFRMWWMLFSFFIKTPQOGAOTRLHCAITGELTILSGNHPSDCHVAVWSAQARNET 300
Db 241 RHSSFRMWWMLFSFFIKTPQOGAOTRLHCAITGELTILSGNHPSDCHVAVWSAQARNET 300
QY 301 IARRLMDVITVTCMASQ 316
Db 301 IARRLMDVITVTCMASQ 316

RESULT 2

US-08-875-273A-2
; Sequence 2, Application US/08875273A
; Patent No. 6106829
; GENERAL INFORMATION:
; APPLICANT: HE, ET AL.
; TITLE OF INVENTION: Human Prostatic Specific Reductase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/875,273A
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,114
; REFERENCE/DOCKET NUMBER: 325800-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-875-273A-2

Query Match 100.0%; Score 1659; DB 3; Length 316;
Best Local Similarity 100.0%; Pred. No. 1,1e-186;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVELMPFLLLLLPFLLYAAAPQIRKMLSSGVCTSTVQLPGKVVVVVTGANTGIGKETAKE 60
Db 1 MVELMPFLLLLLPFLLYAAAPQIRKMLSSGVCTSTVQLPGKVVVVVTGANTGIGKETAKE 60

Db 1 MVELMPFLLLLLPFLLYAAAPQIRKMLSSGVCTSTVQLPGKVVVVVTGANTGIGKETAKE 60
QY 61 LAORGARVYLACRDVEKSELVAKEIOTTGNOQVVRKLDJSDTKSIPAMAKGFAEKH 120
Db 61 LAORGARVYLACRDVEKSELVAKEIOTTGNOQVVRKLDJSDTKSIPAMAKGFAEKH 120
QY 121 LHWINNAGVMMCPYSKTADGFEHMIQVNHJGHFLLTHLLEKLESAPSRIVNSSLAH 180
Db 121 LHWINNAGVMMCPYSKTADGFEHMIQVNHJGHFLLTHLLEKLESAPSRIVNSSLAH 180
QY 181 HLGRIHFHNLQGEKRYNAGLAYCHSKLANILFTQELARLKGSGVTTYVHPGTVOSELY 240
Db 181 HLGRIHFHNLQGEKRYNAGLAYCHSKLANILFTQELARLKGSGVTTYVHPGTVOSELY 240
QY 241 RHSSFRMWWMLFSFFIKTPQOGAOTRLHCAITGELTILSGNHPSDCHVAVWSAQARNET 300
Db 241 RHSSFRMWWMLFSFFIKTPQOGAOTRLHCAITGELTILSGNHPSDCHVAVWSAQARNET 300
QY 301 IARRLMDVITVTCMASQ 316
Db 301 IARRLMDVITVTCMASQ 316

RESULT 3

US-09-123-386-2
; Sequence 2, Application US/09123386
; Patent No. 6344198
; GENERAL INFORMATION:
; APPLICANT: HE, ET AL.
; TITLE OF INVENTION: Human Prostatic Specific Reductase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/123,386
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/464,400
; FILING DATE: JUN-05-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jonathan L. Klein
; REGISTRATION NUMBER: 41,119
; REFERENCE/DOCKET NUMBER: PF150D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-123-386-2

Query Match 100.0%; Score 1659; DB 3; Length 316;
Best Local Similarity 100.0%; Pred. No. 1,1e-186;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVELMPFLLLLLPFLLYAAAPQIRKMLSSGVCTSTVQLPGKVVVVVTGANTGIGKETAKE 60
Db 1 MVELMPFLLLLLPFLLYAAAPQIRKMLSSGVCTSTVQLPGKVVVVVTGANTGIGKETAKE 60

QY 61 LAORGARVYIACRDVEKELVAKEIOTTGNOQVLVRKLDLSDTKSIRAMAKGFAEEKH 120
DB 61 LAORGARVYIACRDVEKELVAKEIOTTGNOQVLVRKLDLSDTKSIRAMAKGFAEEKH 120
QY 121 LHWINNAGVMMCPYSKTADGPEMHIGVNLGHFLTHLLEKLSAPSRIVNVSSLAH 180
DB 121 LHWINNAGVMMCPYSKTADGPEMHIGVNLGHFLTHLLEKLSAPSRIVNVSSLAH 180
QY 181 HLGRIHFHNLQGEKFXNAGLAICHSKLANILFTQELARLKGSGVTTYSVHPGTVOSELY 240
DB 181 HLGRIHFHNLQGEKFXNAGLAICHSKLANILFTQELARLKGSGVTTYSVHPGTVOSELY 240
QY 241 RHSSFMWMMWLFSFFIKTPQOQAOTRLHCALTEGLEILSGNHPSDCHVAVWSAQARNET 300
DB 241 RHSSFMWMMWLFSFFIKTPQOQAOTRLHCALTEGLEILSGNHPSDCHVAVWSAQARNET 300
QY 301 IARRLMDVITVCWASQ 316
DB 301 IARRLMDVITVCWASQ 316

RESULT 4

PCT-US95-01827A-2
Sequence 2, Application PC/TUS9501827A
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Prostatic Specific Reductase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01827A
FILING DATE: Concurrently
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-01827A-2

Query Match 100.0%; Score 1659; DB 5; Length 316;
Best Local Similarity 100.0%; Pred. No. 1,1e-186;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVELMFPILLILLPFLIYMAAPQIRKMLSSGVCTSTVQJPGKVVVVTGANTGIGETAKE 60
DB 1 MVELMFPILLILLPFLIYMAAPQIRKMLSSGVCTSTVQJPGKVVVVTGANTGIGETAKE 60

QY 61 LAORGARVYIACRDVEKELVAKEIOTTGNOQVLVRKLDLSDTKSIRAMAKGFAEEKH 120
DB 61 LAORGARVYIACRDVEKELVAKEIOTTGNOQVLVRKLDLSDTKSIRAMAKGFAEEKH 120
QY 121 LHWINNAGVMMCPYSKTADGPEMHIGVNLGHFLTHLLEKLSAPSRIVNVSSLAH 180
DB 121 LHWINNAGVMMCPYSKTADGPEMHIGVNLGHFLTHLLEKLSAPSRIVNVSSLAH 180
QY 181 HLGRIHFHNLQGEKFXNAGLAICHSKLANILFTQELARLKGSGVTTYSVHPGTVOSELY 240
DB 181 HLGRIHFHNLQGEKFXNAGLAICHSKLANILFTQELARLKGSGVTTYSVHPGTVOSELY 240
QY 241 RHSSFMWMMWLFSFFIKTPQOQAOTRLHCALTEGLEILSGNHPSDCHVAVWSAQARNET 300
DB 241 RHSSFMWMMWLFSFFIKTPQOQAOTRLHCALTEGLEILSGNHPSDCHVAVWSAQARNET 300
QY 301 IARRLMDVITVCWASQ 316
DB 301 IARRLMDVITVCWASQ 316

RESULT 5

US-09-439-313-339
Sequence 339, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Harlock, Jennifer L.
APPLICANT: Harlock, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kados, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.42709
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapien
US-09-439-313-339

Query Match 95.1%; Score 1577; DB 3; Length 318;
Best Local Similarity 98.7%; Pred. No. 5,4e-177;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MVELMFPILLILLPFLIYMAAPQIRKMLSSGVCTSTVQJPGKVVVVTGANTGIGETAKE 60
DB 1 MVELMFPILLILLPFLIYMAAPQIRKMLSSGVCTSTVQJPGKVVVVTGANTGIGETAKE 60
QY 61 LAORGARVYIACRDVEKELVAKEIOTTGNOQVLVRKLDLSDTKSIRAMAKGFAEEKH 120
DB 61 LAORGARVYIACRDVEKELVAKEIOTTGNOQVLVRKLDLSDTKSIRAMAKGFAEEKH 120
QY 121 LHWINNAGVMMCPYSKTADGPEMHIGVNLGHFLTHLLEKLSAPSRIVNVSSLAH 180
DB 121 LHWINNAGVMMCPYSKTADGPEMHIGVNLGHFLTHLLEKLSAPSRIVNVSSLAH 180
QY 181 HLGRIHFHNLQGEKFXNAGLAICHSKLANILFTQELARLKGSGVTTYSVHPGTVOSELY 240
DB 181 HLGRIHFHNLQGEKFXNAGLAICHSKLANILFTQELARLKGSGVTTYSVHPGTVOSELY 240
QY 241 RHSSFMWMMWLFSFFIKTPQOQAOTRLHCALTEGLEILSGNHPSDCHVAVWSAQARNET 300
DB 241 RHSSFMWMMWLFSFFIKTPQOQAOTRLHCALTEGLEILSGNHPSDCHVAVWSAQARNET 300

QY 301 IARRLMDV 308
 Db 301 IARRLMDV 308

RESULT 6

US-09-352-616A-339
 ; Sequence 339, Application US/09352616A
 ; Patent No. 6395278
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Xu, Jiangchun
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
 ; FILE REFERENCE: 210121.427C8
 ; CURRENT APPLICATION NUMBER: US/09/352,616A
 ; CURRENT FILING DATE: 1999-07-13
 ; NUMBER OF SEQ ID NOS: 472
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 339
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-352-616A-339

Query Match 95.1%; Score 1577; DB 3; Length 318;
 Best Local Similarity 98.7%; Pred. No. 5.4e-177;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVELMFPULLLLPFLIYMAAPQIRKMLSSGVCSTVQLPKGVVYVVGANTGIGKETAKE 60
 Db 1 MVELMFPULLLLPFLIYMAAPQIRKMLSSGVCSTVQLPKGVVYVVGANTGIGKETAKE 60
 QY 61 LAQGARVYLACRDEKELVAKETOTTGNOQVLRKLDLSDTKSIRAWAKGFKAEKH 120
 Db 61 LAQGARVYLACRDEKELVAKETOTTGNOQVLRKLDLSDTKSIRAWAKGFKAEKH 120
 QY 121 LHWINNAGVMCPYSKTADGFEMHIGVNLGHFLTHLLLEKLESAPSRIVVSSLAH 180
 Db 121 LHWINNAGVMCPYSKTADGFEMHIGVNLGHFLTHLLLEKLESAPSRIVVSSLAH 180
 QY 181 HLGRHFHNLQGEKFNAGLAICHSKLANILFTQELARRLKSGSVTYSVHPGVQSELY 240
 Db 181 HLGRHFHNLQGEKFNAGLAICHSKLANILFTQELARRLKSGSVTYSVHPGVQSELY 240
 QY 241 RHSSFMRMWMLFSPFIKTPOGAQOTRLHCAITGELIISGNHPSDCHVAVWSAQARNET 300
 Db 241 RHSSFMRMWMLFSPFIKTPOGAQOTSLHCAITGELIISGNHPSDCHVAVWSAQARNET 300
 QY 301 IARRLMDV 308
 Db 301 IARRLMDV 308

RESULT 7

US-09-636-215-339
 ; Sequence 339, Application US/09636215
 ; Patent No. 6620922
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.
 APPLICANT: Vedvick, Thomas S.
 APPLICANT: Carter, Derrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.4271C17
 ; CURRENT APPLICATION NUMBER: US/09/636,215
 ; CURRENT FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 852
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 339
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-636-215-339

Query Match 95.1%; Score 1577; DB 4; Length 318;
 Best Local Similarity 98.7%; Pred. No. 5.4e-177;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVELMFPULLLLPFLIYMAAPQIRKMLSSGVCSTVQLPKGVVYVVGANTGIGKETAKE 60
 Db 1 MVELMFPULLLLPFLIYMAAPQIRKMLSSGVCSTVQLPKGVVYVVGANTGIGKETAKE 60
 QY 61 LAQGARVYLACRDEKELVAKETOTTGNOQVLRKLDLSDTKSIRAWAKGFKAEKH 120
 Db 61 LAQGARVYLACRDEKELVAKETOTTGNOQVLRKLDLSDTKSIRAWAKGFKAEKH 120
 QY 121 LHWINNAGVMCPYSKTADGFEMHIGVNLGHFLTHLLLEKLESAPSRIVVSSLAH 180
 Db 121 LHWINNAGVMCPYSKTADGFEMHIGVNLGHFLTHLLLEKLESAPSRIVVSSLAH 180
 QY 181 HLGRHFHNLQGEKFNAGLAICHSKLANILFTQELARRLKSGSVTYSVHPGVQSELY 240
 Db 181 HLGRHFHNLQGEKFNAGLAICHSKLANILFTQELARRLKSGSVTYSVHPGVQSELY 240
 QY 241 RHSSFMRMWMLFSPFIKTPOGAQOTRLHCAITGELIISGNHPSDCHVAVWSAQARNET 300
 Db 241 RHSSFMRMWMLFSPFIKTPOGAQOTSLHCAITGELIISGNHPSDCHVAVWSAQARNET 300
 QY 301 IARRLMDV 308
 Db 301 IARRLMDV 308

RESULT 8

US-09-685-166A-339
 ; Sequence 339, Application US/09685166A
 ; Patent No. 6630305
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 339
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapien
US-09-685-166A-339

Query Match 95.1%; Score 1577; DB 4; Length 318;
Best Local Similarity 98.7%; Pred. No. 5,4e-177;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVELMFPILLILLPFLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGKETAKE 60
DB 1 MVELMFPILLILLPFLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGKETAKE 60
QY 61 LAQGARVYLAQDVEKELVAKEIQTTGNOQVLRKLDLSDTKSIRAPAKGFLEBEKH 120
DB 61 LAQGARVYLAQDVEKELVAKEIQTTGNOQVLRKLDLSDTKSIRAPAKGFLEBEKH 120
QY 121 LHWVNNAGVMMCPYSKTADGFEHIGVNHGFLTLHLLLEKESAPSRIVVSSLAH 180
DB 121 LHWVNNAGVMMCPYSKTADGFEHIGVNHGFLTLHLLLEKESAPSRIVVSSLAH 180
QY 181 HLGRHFHNLQGEKRYNAGLAYCHSKLANILFTQELARLKSGVTTYVHPGTVOSELV 240
DB 181 HLGRHFHNLQGEKRYNAGLAYCHSKLANILFTQELARLKSGVTTYVHPGTVOSELV 240
QY 241 RHSSFWRMWMLFSFFIKTPQOQAOTRLHCAITBGLJILSGNHSDDCHVAVWSAQAARNET 300
DB 241 RHSSFWRMWMLFSFFIKTPQOQAOTSLHCAITBGLJILSGNHSDDCHVAVWSAQAARNET 300
QY 301 IARRLMDV 308
DB 301 IARRLMDV 308

RESULT 9
US-09-679-426-339
Sequence 339, Application US/09679426
Patent No. 6759515
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kales, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 339
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapien

US-09-679-426-339

Query Match 95.1%; Score 1577; DB 4; Length 318;
Best Local Similarity 98.7%; Pred. No. 5,4e-177;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVELMFPILLILLPFLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGKETAKE 60
DB 1 MVELMFPILLILLPFLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGKETAKE 60
QY 61 LAQGARVYLAQDVEKELVAKEIQTTGNOQVLRKLDLSDTKSIRAPAKGFLEBEKH 120
DB 61 LAQGARVYLAQDVEKELVAKEIQTTGNOQVLRKLDLSDTKSIRAPAKGFLEBEKH 120
QY 121 LHWVNNAGVMMCPYSKTADGFEHIGVNHGFLTLHLLLEKESAPSRIVVSSLAH 180
DB 121 LHWVNNAGVMMCPYSKTADGFEHIGVNHGFLTLHLLLEKESAPSRIVVSSLAH 180
QY 181 HLGRHFHNLQGEKRYNAGLAYCHSKLANILFTQELARLKSGVTTYVHPGTVOSELV 240
DB 181 HLGRHFHNLQGEKRYNAGLAYCHSKLANILFTQELARLKSGVTTYVHPGTVOSELV 240
QY 241 RHSSFWRMWMLFSFFIKTPQOQAOTRLHCAITBGLJILSGNHSDDCHVAVWSAQAARNET 300
DB 241 RHSSFWRMWMLFSFFIKTPQOQAOTSLHCAITBGLJILSGNHSDDCHVAVWSAQAARNET 300
QY 301 IARRLMDV 308
DB 301 IARRLMDV 308

RESULT 10
US-09-270-767-41724
Sequence 41724, Application US/09270767
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 41724
LENGTH: 309
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURES:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41724

Query Match 30.9%; Score 512.5; DB 4; Length 309;
Best Local Similarity 41.4%; Pred. No. 1.7e-101;
Matches 113; Conservative 55; Mismatches 102; Indels 3; Gaps 2;

QY 38 QLPGRVYVVTGANTGIGKETAKELAQRARVYIACDVEKELVAKEIQTTGNOQVLR 97
DB 38 QLPGRVYVVTGANTGIGKETAKELAQRARVYIACDVEKELVAKEIQTTGNOQVLR 97
QY 22 XMEGKTVIITGANGSIGKETAKDLAQRARVYIACDVEKELVAKEIQTTGNOQVLR 81
DB 22 XMEGKTVIITGANGSIGKETAKDLAQRARVYIACDVEKELVAKEIQTTGNOQVLR 81
QY 98 KLDLSDTKSIRAPAKGFLEBEKHILHWVNNAGVMMCPYSKTA-DGFEHIGVNHGFL 156
DB 98 KLDLSDTKSIRAPAKGFLEBEKHILHWVNNAGVMMCPYSKTA-DGFEHIGVNHGFL 156
QY 82 KLDLSDTKSIRAPAKGFLEBEKHILHWVNNAGVMMCPYSKTA-DGFEHIGVNHGFL 141
DB 82 KLDLSDTKSIRAPAKGFLEBEKHILHWVNNAGVMMCPYSKTA-DGFEHIGVNHGFL 141
QY 157 THLLLEKESAPSRIVVSSLAHILGRHFHNLQGEKRYNAGLAYCHSKLANILFTQEL 216
DB 157 THLLLEKESAPSRIVVSSLAHILGRHFHNLQGEKRYNAGLAYCHSKLANILFTQEL 216
QY 142 THLLIDVKKSAAPARIVYVASELYRLSSVLAINDIGTPPAVLYVSKRFANIYFAR 201
DB 142 THLLIDVKKSAAPARIVYVASELYRLSSVLAINDIGTPPAVLYVSKRFANIYFAR 201
QY 217 ARLKSGVTTYVHPGTVOSELVHRSSF--VMMWMLFSFFIKTPQOQAOTRLHCAIT 274
DB 217 ARLKSGVTTYVHPGTVOSELVHRSSF--VMMWMLFSFFIKTPQOQAOTRLHCAIT 274
QY 202 AKRLGKTVVNTFLHREMIDSGIWRVPPFLNIPMAAITGPFKTKAKAGQITVIATSD 261
DB 202 AKRLGKTVVNTFLHREMIDSGIWRVPPFLNIPMAAITGPFKTKAKAGQITVIATSD 261
QY 275 GLEILSGNHSDDCHVAVWSAQAARNETIARRLMDV 307
DB 275 GLEILSGNHSDDCHVAVWSAQAARNETIARRLMDV 307

Db 262 EVANYSKYMDCENTINAAALDEKGLKWE 294

RESULT 11
US-08-580-545B-2

Sequence 2, Application US/08580545B
Patent No. 5932713

GENERAL INFORMATION:

APPLICANT: Yoshihisa, Kasukabe

APPLICANT: Koichi, Fujisawa

APPLICANT: Susumu, Nishiguchi

APPLICANT: Yoshiko, Maekawa

APPLICANT: Randy, Allen

TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 601 Thirteenth Street, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/580,545B

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Bretschneider, Barry E.

REGISTRATION NUMBER: 28,055

REFERENCE/DOCKET NUMBER: 04473/068001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/783-5070

TELEFAX: 202/783-2331

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 323 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-580-545B-2

Query Match

Best Local Similarity 29.8%; Score 494.5; DB 2; Length 323;

Best Local Similarity 40.1%; Pred. No. 2.5e-49;

Matches 110; Conservative 53; Mismatches 100; Indels 11; Gaps 4;

Db 45 VTGANTGIGKETAKELAQGARYVYACRDVEKGEIVAKETQTTGNQGVLYRKLDSDT 104

Db 38 LVTGASGIGLETSRVYALRGVYIIGARNKMAANEKXIVENPRARIDVLELDLST 97

Db 105 KSIRAMAKGFYAEKELHVMINNAVVMCPYKTDGFEHIGVNLGHFLTLHLLEKL 164

Db 98 NSIRSFADNFIALHLPINILINNAVIMFCFQLSQNGLEVOFATNHIGHFLTLNLLDTM 157

Db 165 KESAPS-----RIVNVSSLAH---HGRIFHNLOGEKFTYNAGLAYCHSKLANILFTQEL 216

Db 158 KNTVKATGIGRGVYVNISSIAHNYCYKKGIRFEKINDKOGYSEKRAVGOSEKLANILHANEL 217

Db 217 ARRLKSGV--TIVSVHPTGVQSELVRHSSFMKMMWLFSFPI-KTPOGAGQTRLHCALT 273

Db 218 SRRLQEGVNIIVTVSVHPTGLIMTPLFRHSADLMKLLKFFSFLMKVVPQGAATTCYVALH 277

Db 274 EGLEILSGNHFSDCHVAVWSAQARNETIARLMD 307

Db 278 PRLNGVTGKYFADCNEMRPSVARNBSLGRLEWE 311

RESULT 12

US-09-262-653A-2

Sequence 2, Application US/09262653A
Patent No. 6166294

GENERAL INFORMATION:

APPLICANT: Yoshihisa, Kasukabe

APPLICANT: Koichi, Fujisawa

APPLICANT: Susumu, Nishiguchi

APPLICANT: Yoshiko, Maekawa

APPLICANT: Randy, Allen

TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 601 Thirteenth Street, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/262,653A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Bretschneider, Barry E.

REGISTRATION NUMBER: 28,055

REFERENCE/DOCKET NUMBER: 04473/068001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/783-5070

TELEFAX: 202/783-2331

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 323 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-262-653A-2

Query Match

Best Local Similarity 29.8%; Score 494.5; DB 3; Length 323;

Best Local Similarity 40.1%; Pred. No. 2.5e-49;

Matches 110; Conservative 53; Mismatches 100; Indels 11; Gaps 4;

Db 45 VTGANTGIGKETAKELAQGARYVYACRDVEKGEIVAKETQTTGNQGVLYRKLDSDT 104

Db 38 LVTGASGIGLETSRVYALRGVYIIGARNKMAANEKXIVENPRARIDVLELDLST 97

Db 105 KSIRAMAKGFYAEKELHVMINNAVVMCPYKTDGFEHIGVNLGHFLTLHLLEKL 164

Db 98 NSIRSFADNFIALHLPINILINNAVIMFCFQLSQNGLEVOFATNHIGHFLTLNLLDTM 157

Db 165 KESAPS-----RIVNVSSLAH---HGRIFHNLOGEKFTYNAGLAYCHSKLANILFTQEL 216

Db 158 KNTVKATGIGRGVYVNISSIAHNYCYKKGIRFEKINDKOGYSEKRAVGOSEKLANILHANEL 217

Db 217 ARRLKSGV--TIVSVHPTGVQSELVRHSSFMKMMWLFSFPI-KTPOGAGQTRLHCALT 273

Db 218 SRRLQEGVNIIVTVSVHPTGLIMTPLFRHSADLMKLLKFFSFLMKVVPQGAATTCYVALH 277

Db 274 EGLEILSGNHFSDCHVAVWSAQARNETIARLMD 307

Db 278 PRLNGVTGKYFADCNEMRPSVARNBSLGRLEWE 311

RESULT 13

US-09-489-847-182

Sequence 182, Application US/09489847

Patent No. 6476195

GENERAL INFORMATION:

APPLICANT: Rosen et al

TITLE OF INVENTION: 98 Human Secreted Proteins

```

; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-04-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 182
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (38)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (247)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-489-847-182

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Query Match 28.6%; Score 474; DB 4; Length 330;

Best Local Similarity 39.6%; Pred. No. 6.7e-47; Matches 114; Conservative 43; Mismatches 97; Indels 34; Gaps 7;

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QY 40 PGKVVVVGANTGIGKETAKELAORGARVYLACDVKELVAKEIQTTGNOQVLRKL 99
DB 42 PDRVAIVTGTGDTGIGYSPAKHLARLGNHVIAGNDSKAKQVSKIEETLNDKVEPLYC 101
QY 100 DLSOTKIRAWAKGFKAEKHLHWINNAGVMCPYSKTADGFEHMGVNHGFLITHL 159
DB 102 DLAHTSTIRQVQFKMKKIPHLVILNAGVMVPCRKTRDGFEEHGLVYLGHFLITNL 161
QY 160 LLEKLKESA-----PSRIYVSSLAHGRIFHNLIQGEKFNAGLACHSKLANILPTOE 215
DB 162 LLDLTKEGSGPGHARVTVSSATHYVAELNMDLOSACSPRAAQAQSKLALVLTTH 221
QY 216 LARRL--KSGVTTYVAPGTVOSELVHSSFMKRM-----WWLFSEFIKTPQOGA 264
DB 222 LQRLAAGSHVTVANVDPGVVNTDXYKH--VFMAIRLAKKLIGWLLF---KTPDEGA 274
QY 265 QTRHLCAITGELISGNHF-----SDCHVAMVSAQARNETIARRLM 306
DB 275 WTSIYAATPELLEGVGRVLYNEKETKSLHVTY-----NOKLQOOLM 316

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RESULT 14

US-08-530-165-7

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; Sequence 7, Application US/08530165
; Patent No. 5907081
; GENERAL INFORMATION:
; APPLICANT: Isaac, Peter G.
; APPLICANT: Roberts, Jeremy A.
; APPLICANT: Coupe, Simon A.
; TITLE OF INVENTION: Control of Plant Abscission and Pod Dehiscence
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: 20005
; ZIP: USA

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,165
; FILING DATE: 29-SEP-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/00689
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9306726.2
; FILING DATE: 31-MAR-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2500
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-530-165-7

```

Query Match 28.1%; Score 466.5; DB 2; Length 320;

Best Local Similarity 38.9%; Pred. No. 4.9e-46; Matches 111; Conservative 48; Mismatches 115; Indels 11; Gaps 4;

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QY 34 TSTVQLPGKVVVVGANTGIGKETAKELAORGARVYLACDVKELVAKEIQTTGNOQ 93
DB 26 TSHDAKHUTAITITGTSIGLEAARVLGMRGAHYIISRNTKANDSKEMILQVTPNR 85
QY 94 VLVRLKLDSDTKSIRAWAKGFKAEKHLHWINNAGVMCPYSKTADGFEHMGVNHGCH 153
DB 86 ICDGLDLSISIKSVSFHFQFLANVPLNIIINNAGVMCPQLSEDDIGESQFATNHIGH 145
QY 154 FLTHLLEKLKESA-----PSRIYVSSLAH--HGRIFHNLIQGEKFNAGLACHS 205
DB 146 FLTHLLEKLKESA-----PSRIYVSSLAH--HGRIFHNLIQGEKFNAGLACHS 205
QY 206 KLANILFTOLARPKSGV--TTSVHPGTVOSELVHSSFMKRMWWLFSEFIKTPQO 262
DB 206 KLANILHSAALRSKIQEBSVNTINSVHGILITTLFHSHGVMVLAAMSFFLKNIPQ 265
QY 263 GAQTRHLCAITGELISGNHPSDCHVAMVSAQARNETIARRLM 307
DB 266 GAATCYVALHPDLKDVTKGYFADCNVTPSNFATDTTLADKLWD 310

```

RESULT 15

US-09-489-847-330

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; Sequence 330, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06

```

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: NUMBER OF SEQ ID NOS: 376
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 330
: LENGTH: 350
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (38)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (247)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-03-489-847-330

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 18:01:08 ; Search time 156 Seconds
(without alignments)
726.657 Million cell updates/sec

Title: US-10-021-002-2
Perfect score: 1659
Sequence: 1 MVELMFPLLLLLPFLLYMA.....RNFTIARRLMDVITQWASQ 316

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_23Sep04.*
2: geneseqp1980s.*
3: geneseqp1990s.*
4: geneseqp2000s.*
5: geneseqp2001s.*
6: geneseqp2002s.*
7: geneseqp2003as.*
8: geneseqp2003bs.*
9: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1652	99.6	316	2 AAW03198	AAW03198 Prostate
2	1577	95.1	318	3 AAY82014	AAY82014 Human imm
3	1577	95.1	318	3 AAB12158	AAB12158 Hydrophob
4	1577	95.1	318	4 AAM01129	AAM01129 Human pro
5	1577	95.1	318	4 AAM93777	AAM93777 Human pro
6	1577	95.1	318	4 AAB74812	AAB74812 Prostate
7	1577	95.1	318	4 AAG99014	AAG99014 Human pro
8	1577	95.1	318	4 AAB71665	AAB71665 Prostate
9	1577	95.1	318	5 AAB96858	AAB96858 Human pro
10	1577	95.1	318	5 ABB95234	ABB95234 Human pro
11	1577	95.1	318	6 ABR54346	ABR54346 Prostate
12	1577	95.1	318	7 ADB75403	ADB75403 Prostate
13	1577	95.1	318	7 ADB13789	ADB13789 Human pro
14	1577	95.1	318	7 ADG26205	ADG26205 Human pro
15	1577	95.1	318	7 ADJ71200	ADJ71200 Human hea
16	1577	95.1	318	8 ADI06507	ADI06507 Human tum
17	1577	95.1	318	8 ADI31755	ADI31755 Human pro
18	1577	95.1	318	8 AAY48616	AAY48616 Human bre
19	1577	95.1	318	7 ABR63833	ABR63833 Human oxi
20	1573	94.8	318	7 ABR82986	ABR82986 Human CGI
21	1573	94.8	318	7 AAB36900	AAB36900 Human ARS
22	1555	93.7	314	8 ADH45298	ADH45298 Human enz
23	1169	70.1	248	8 ADA54192	ADA54192 Human pro
24	1130	68.1	316	6 ABR82985	ABR82985 Human umm
25	1130	68.1	316	7 ABR82985	ABR82985 Human umm

26	1129	68.1	316	5 AAE14438	AAE14438 Human dru
27	1117.5	67.4	321	5 ABB69268	ABB69268 Human pol
28	1112	67.0	260	7 ADG76361	ADG76361 Human inc
29	1020	61.5	278	6 ABB52578	ABB52578 Human NOV
30	805	48.6	246	4 AAB73685	AAB73685 Human oxi
31	728	43.9	300	4 ABB58826	ABB58826 Drosophi
32	726	43.8	296	4 ABB58831	ABB58831 Drosophi
33	706.5	42.6	331	4 AAB88356	AAB88356 Human mem
34	705.5	42.5	331	3 AAY93722	AAY93722 Human PRO
35	705.5	42.5	331	4 AAB66121	AAB66121 Protein o
36	705.5	42.5	331	4 AAE05174	AAE05174 Human dru
37	705.5	42.5	331	6 AAB37278	AAB37278 Human gen
38	705.5	42.5	331	6 ABO33614	ABO33614 Novel hum
39	705.5	42.5	331	7 ABO44467	ABO44467 Human sec
40	705.5	42.5	331	7 ABO33491	ABO33491 Novel hum
41	705.5	42.5	331	7 ADC17985	ADC17985 Human PRO
42	705.5	42.5	331	7 ADD70631	ADD70631 Human sec
43	705.5	42.5	331	7 ADD39708	ADD39708 Human sec
44	705.5	42.5	331	7 ADD70154	ADD70154 Human sec
45	705.5	42.5	331	7 ADD38275	ADD38275 Human sec

ALIGNMENTS

RESULT 1
ID AAW03198 standard; protein; 316 AA.
XX AAW03198;
AC AAW03198;
DT 26-FEB-1997 (first entry)
DE Prostate specific reductase.
XX Prostate specific reductase; human; prostate; prostate cancer; inhibitor;
XX antagonist; cancer metastasis; prostate disorder; antibody; therapy; PSR;
XX prostate cancer vaccine.
XX Homo sapiens.
OS
XX
XX WO9622360-A1.
XX
XX 25-JUL-1996.
XX
XX 20-JAN-1995; 95WO-US001827.
XX
XX 20-JAN-1995; 95WO-US001827.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX He W, Weisner PS, Hudson PL, Rosen CA;
PI WPI, 1996-354517/35.
DR N-PSDB; AAT91321.
XX
XX Human prostate specific reductase - useful for diagnosing and treating
PT prostate cancer and screening new antagonists.
XX
XX Claim 19; Page 44-45; 57pp; English.
XX
XX This sequence represents the human prostate specific reductase (PSR). PSR
XX genes are present in all cells of the body, however transcription and
XX expression of PSR is limited to the prostate in normal individuals. When
XX prostate cancer is present, the cancer cells migrate and cause other
XX cells to begin expressing PSR. It is therefore thought that the presence
XX of mRNA encoding PSR in cells of the host (other than those derived from
XX the prostate) is indicative of prostate cancer metastases. The DNA
XX of PSR provides a diagnostic marker for prostate disorders. The DNA
XX encoding this sequence can therefore be used to diagnose metastasis of
XX prostate cancer cells. PSR may be used to screen for PSR antagonists,
XX which can then be used as inhibitors of PSR expression. Antibodies
XX against this protein sequence can be used to target prostate cells, and

CC could also be used as part of a prostate cancer vaccine
 XX Sequence 316 AA;

Query Match 99.6%; Score 1652; DB 2; Length 316;
 Best Local Similarity 99.7%; Pred. No. 9.1e-163;
 Matches 315; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVELMFPLLLLPFLYMAAPQIRKMLSSGVCSTVQLGKVVVVGANTGIGKETAKE 60
 DB 1 MVELMFPLLLLPFLYMAAPQIRKMLSSGVCSTVQLGKVVVVGANTGIGKETAKE 60
 QY 61 LAQSGARYYLAACRDVEKGEIVAKEIQTTGNQVLYVKLDLSDTKSIRAWAKGFKAEEKH 120
 DB 61 LAQSGARYYLAACRDVEKGEIVAKEIQTTGNQVLYVKLDLSDTKSIRAWAKGFKAEEKH 120
 QY 121 LHWNNAGVMMCCYSTADGFEMHIGVNLGHFLTHLLLEKLEKESAPRIVVSSLAH 180
 DB 121 LHWNNAGVMMCCYSTADGFEMHIGVNLGHFLTHLLLEKLEKESAPRIVVSSLAH 180
 QY 181 HLGRHFNHLOGEKFYNAGLAYCHSKLANILFTQELARRLKSGSVTTSVHPGTVOSELY 240
 DB 181 HLGRHFNHLOGEKFYNAGLAYCHSKLANILFTQELARRLKSGSVTTSVHPGTVOSELY 240
 QY 241 RHSSFMKMMWTLSEFFIKTPQOGAQTFLHCAITBGLFISGNHPSDCHVAVSAQARNET 300
 DB 241 RHSSFMKMMWTLSEFFIKTPQOGAQTFLHCAITBGLFISGNHPSDCHVAVSAQARNET 300
 QY 301 IARLMDVITVCMASQ 316
 DB 301 IARLMDVITVCMASQ 316

RESULT 2
 AAY82014
 ID AAY82014 standard; protein; 318 AA.

AC AAY82014;
 DT 13-JUN-2000 (first entry)
 XX Human immunogenic prostate tumour protein sequence SEQ ID NO:339.
 DE Human immunogenic prostate tumour protein sequence SEQ ID NO:339.
 XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
 KW immunogenic; cytostatic; vaccine.
 XX Homo sapiens.

OS Homo sapiens.
 PN WO200004149-A2.
 XX 27-JAN-2000.

PF 14-JUL-1999; 99WO-US015838.
 XX 14-JUL-1998; 98US-00115453.
 PR 14-JUL-1998; 98US-00116134.
 PR 23-SEP-1998; 98US-00158812.
 PR 23-SEP-1998; 98US-00158822.
 PR 15-JAN-1999; 99US-00232149.
 PR 15-JAN-1999; 99US-00232880.
 PR 09-APR-1999; 99US-00288946.

XX (CORI-) CORIXA CORP.

PI Dillon DC, Harlocker SL, Yudin J, Xu J, Mitcham JL;
 DR WPI, 2000-171268/15.

XX New polypeptide useful for treating and diagnosing prostate cancer
 PT comprises an immunogenic portion of prostate tumor protein.
 XX Claim 3; Page 209-210; 263pp; English.

CC The present invention describes isolated polypeptides, comprising an
 CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
 CC and polynucleotides encoding them have cytostatic activity and can be
 CC used in vaccines and in gene therapy. The polypeptides and
 CC polynucleotides encoding them, antigen presenting cells which express the
 CC polypeptides, antibodies against the polypeptides and vaccines comprising
 CC them can be used for inhibiting the development of prostate cancer in a
 CC patient. The polypeptides can be used to generate antibodies or anti-
 CC idiotypic antibodies for passive immuno therapy. A portion of the
 CC polynucleotides encoding the polypeptides can be used as a probe or to
 CC modulate the expression of the polypeptides. AA062241 to AA06591 and
 CC AAY82000 to AAY82020 represent sequences used in the exemplification of
 CC the present invention

Sequence 318 AA;

Query Match 95.1%; Score 1577; DB 3; Length 318;
 Best Local Similarity 98.7%; Pred. No. 5.9e-155;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVELMFPLLLLPFLYMAAPQIRKMLSSGVCSTVQLGKVVVVGANTGIGKETAKE 60
 DB 1 MVELMFPLLLLPFLYMAAPQIRKMLSSGVCSTVQLGKVVVVGANTGIGKETAKE 60
 QY 61 LAQSGARYYLAACRDVEKGEIVAKEIQTTGNQVLYVKLDLSDTKSIRAWAKGFKAEEKH 120
 DB 61 LAQSGARYYLAACRDVEKGEIVAKEIQTTGNQVLYVKLDLSDTKSIRAWAKGFKAEEKH 120
 QY 121 LHWNNAGVMMCCYSTADGFEMHIGVNLGHFLTHLLLEKLEKESAPRIVVSSLAH 180
 DB 121 LHWNNAGVMMCCYSTADGFEMHIGVNLGHFLTHLLLEKLEKESAPRIVVSSLAH 180
 QY 181 HLGRHFNHLOGEKFYNAGLAYCHSKLANILFTQELARRLKSGSVTTSVHPGTVOSELY 240
 DB 181 HLGRHFNHLOGEKFYNAGLAYCHSKLANILFTQELARRLKSGSVTTSVHPGTVOSELY 240
 QY 241 RHSSFMKMMWTLSEFFIKTPQOGAQTFLHCAITBGLFISGNHPSDCHVAVSAQARNET 300
 DB 241 RHSSFMKMMWTLSEFFIKTPQOGAQTFLHCAITBGLFISGNHPSDCHVAVSAQARNET 300
 QY 301 IARLMDV 308
 DB 301 IARLMDV 308

RESULT 3
 AAB12158
 ID AAB12158 standard; protein; 318 AA.

AC AAB12158;
 DT 02-FEB-2001 (first entry)
 XX Hydrophobic domain protein isolated from HT-1080 cells.
 DE Hydrophobic domain protein isolated from HT-1080 cells.

KW Human; secreted protein; membrane protein; hydrophobic domain;
 KW proliferation control; differentiation induction; material transport;
 KW biophysics; signal receptor; ion channel; transporter; immunostimulant;
 KW immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
 KW autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.

XX Homo sapiens.

PI WO200029448-A2.
 XX 25-MAY-2000.

PF 17-NOV-1999; 99WO-JF006412.

XX 17-NOV-1998; 98UP-00326255.
 PR 22-DEC-1998; 98UP-00364315.
 PR 16-MAR-1999; 99JP-00069811.

27-APR-1999; 99JP-00119299.
 19-MAY-1999; 99JP-00138169.
 (SAGA) SAGAMI CHEM RES CENT.
 (PROT-) PROTEGENE INC.
 Kato S, Kimura T;
 WPI; 2000-387753/33.
 N-PSDB; AAA62061, AAA62071.
 proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic.
 Claim 1; Page 369-370; 410pp; English.
 Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophysics of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is a human protein which has at least one hydrophobic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haemopoiesis activity, tissue growth activity, haemostatic activity/inhibin activity, chemotactic/chemokinetic activity, and tumour and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present protein could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's disease, and cancer
 Sequence 318 AA:
 Query Match 95.1%; Score 1577; DB 3; Length 318;
 Best Local Similarity 98.7%; Pred. No. 5.9e-155;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MVELMFPILLLLPFLVMAAPQIRKMLSSGVTSTVQLPKRVVVTGANTGIGKETAKE 60
 DB 1 MVELMFPILLLLPFLVMAAPQIRKMLSSGVTSTVQLPKRVVVTGANTGIGKETAKE 60
 QY 61 LAQGRARYLAACRDVEKELVAKEIQTTGNQOVLVRKLDLSDTKSIRAMAKGFABEEKH 120
 DB 61 LAQGRARYLAACRDVEKELVAKEIQTTGNQOVLVRKLDLSDTKSIRAFAGFLAEEKH 120
 QY 121 LHWINNAGVMWCPYSKTADGFEHMGVNHGHEFLTHLLLEKLESAPSRIVNSSLAH 180
 DB 121 LHWINNAGVMWCPYSKTADGFEHMGVNHGHEFLTHLLLEKLESAPSRIVNSSLAH 180
 QY 181 HLGRIHFHNLQGEKFNAGLAVCHSKLANILFTQELARLKSGVTTYSVHPGTQSELY 240
 DB 181 HLGRIHFHNLQGEKFNAGLAVCHSKLANILFTQELARLKSGVTTYSVHPGTQSELY 240
 QY 241 RHSSFWRMWMLFSPFIKTPOQAGOTRLHCALTEGLTILSGNHFSDCHVAWVSAQARNET 300
 DB 241 RHSSFWRMWMLFSPFIKTPOQAGOTSLHCALTEGLTILSGNHFSDCHVAWVSAQARNET 300
 QY 301 IARRLMVDV 308
 DB 301 IARRLMVDV 308
 RESULT 4
 AAM01129
 ID AAM01129 standard; protein; 318 AA.
 AC AAM01129;
 XX 04-OCT-2001 (first entry)
 DT Human prostate-specific amino acid sequence P5095.
 XX

Human; prostate cancer; prostate-specific; diagnosis; vaccine;
 cytostatic; gene therapy; metastasis.
 Homo sapiens.
 WO200151633-A2.
 19-JUL-2001.
 16-JAN-2001; 2001WO-US001574.
 14-JAN-2000; 2000US-00483672.
 (CORI-) CORIXA CORP.
 Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
 Kalos MD, Fanger GR, Day CH, Rector MM, Stolk JA, Skeiky YAM;
 Wang A, Weagner MJ;
 WPI; 2001-425873/45.
 New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines.
 Claim 2; Page 335; 543pp; English.
 The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), 'antibodies to (I) or (II) are used to treat cancer in a patient. (I) and (II) are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH3357 to AAH3944 and AAM0115 to AAM0138 represent polynucleotide and amino acid sequences used in the exemplification of the present invention
 Sequence 318 AA:
 Query Match 95.1%; Score 1577; DB 4; Length 318;
 Best Local Similarity 98.7%; Pred. No. 5.9e-155;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MVELMFPILLLLPFLVMAAPQIRKMLSSGVTSTVQLPKRVVVTGANTGIGKETAKE 60
 DB 1 MVELMFPILLLLPFLVMAAPQIRKMLSSGVTSTVQLPKRVVVTGANTGIGKETAKE 60
 QY 61 LAQGRARYLAACRDVEKELVAKEIQTTGNQOVLVRKLDLSDTKSIRAMAKGFABEEKH 120
 DB 61 LAQGRARYLAACRDVEKELVAKEIQTTGNQOVLVRKLDLSDTKSIRAFAGFLAEEKH 120
 QY 121 LHWINNAGVMWCPYSKTADGFEHMGVNHGHEFLTHLLLEKLESAPSRIVNSSLAH 180
 DB 121 LHWINNAGVMWCPYSKTADGFEHMGVNHGHEFLTHLLLEKLESAPSRIVNSSLAH 180
 QY 181 HLGRIHFHNLQGEKFNAGLAVCHSKLANILFTQELARLKSGVTTYSVHPGTQSELY 240
 DB 181 HLGRIHFHNLQGEKFNAGLAVCHSKLANILFTQELARLKSGVTTYSVHPGTQSELY 240
 QY 241 RHSSFWRMWMLFSPFIKTPOQAGOTRLHCALTEGLTILSGNHFSDCHVAWVSAQARNET 300
 DB 241 RHSSFWRMWMLFSPFIKTPOQAGOTSLHCALTEGLTILSGNHFSDCHVAWVSAQARNET 300
 QY 301 IARRLMVDV 308
 DB 301 IARRLMVDV 308

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RESULT 5
AA093777
ID AA093777 standard; protein, 318 AA.
XX
AC AA093777;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 3788.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
EN Bp130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
XX
PR 11-JAN-2000; 2000JP-00118774.
XX
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Oka T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
XX
DR N-PSDB; AAK94732.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Claim 8; SEQ ID NO 3788; 1380bp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5' and 3' ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 318 AA;
XX
Query Match 95.1%; Score 1577; DB 4; Length 318;
Best Local Similarity 98.7%; Pred. No. 5.9e-155;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 MVELMPFLILLIPFLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKE 60
DB 1 MVELMPFLILLIPFLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKE 60
XX
QY 1 LARGARVYLACGADVKGELVAKELIOTGGNOOVYRKLDSDTSIRAFAGFLAESEKH 120
DB 1 LARGARVYLACGADVKGELVAKELIOTGGNOOVYRKLDSDTSIRAFAGFLAESEKH 120
XX
QY 121 LHWYNNAGVMGCPYSKTDGFEHMGVNHGFLTLHLLEKLESAPSRIYVNSLAH 180
DB 121 LHWYNNAGVMGCPYSKTDGFEHMGVNHGFLTLHLLEKLESAPSRIYVNSLAH 180
XX
QY 121 LHWYNNAGVMGCPYSKTDGFEHMGVNHGFLTLHLLEKLESAPSRIYVNSLAH 180
DB 121 LHWYNNAGVMGCPYSKTDGFEHMGVNHGFLTLHLLEKLESAPSRIYVNSLAH 180
XX
QY 181 HLGRIHFPHNLQGRKFVNAAGLACHSKLANILFTQELARLKSSGTTYSVHPGTVOSELV 240
DB 181 HLGRIHFPHNLQGRKFVNAAGLACHSKLANILFTQELARLKSSGTTYSVHPGTVOSELV 240
XX
QY 241 RHSEFMRMMWMLFSFFIKTPQOGAOTSLHCAITGELTSLGNSHNFSDCHVAVWSAQARNET 300
DB 241 RHSEFMRMMWMLFSFFIKTPQOGAOTSLHCAITGELTSLGNSHNFSDCHVAVWSAQARNET 300

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DB 241 RHSEFMRMMWMLFSFFIKTPQOGAOTSLHCAITGELTSLGNSHNFSDCHVAVWSAQARNET 300
QY 301 IARRLMDV 308
DB 301 IARRLMDV 308
XX
RESULT 6
AA069774
ID AA069774 standard; protein, 318 AA.
XX
AC AA069774;
XX
DT 30-JAN-2002 (first entry)
XX
DE Human prostate cDNA encoded protein #12.
XX
KW Human; prostate cancer; cytostatic; immunosuppressant; tumour; immunogen.
XX
OS Homo sapiens.
XX
EN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009919.
XX
PR 27-MAR-2000; 2000US-00536857.
XX
PR 09-MAY-2000; 2000US-00568100.
XX
PR 12-MAY-2000; 2000US-00570737.
XX
PR 13-JUN-2000; 2000US-00593793.
XX
PR 27-JUN-2000; 2000US-00605783.
XX
PR 09-AUG-2000; 2000US-00636215.
XX
PR 29-AUG-2000; 2000US-00651236.
XX
PR 06-SEP-2000; 2000US-00657279.
XX
PR 02-OCT-2000; 2000US-00679426.
XX
PR 10-OCT-2000; 2000US-00685166.
XX
PR 09-NOV-2000; 2000US-00709729.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MM, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer.
XX
PS Claim 2; Page 337; 579bp; English.
XX
CC The invention relates to isolated prostate-specific polynucleotides,
CC polypeptides, fusion proteins of the polypeptides, antibodies raised
CC against the polypeptides (or antigenic epitopes derived from them) and
CC antigen-presenting cells expressing the polypeptides. The antibodies are
CC useful for detecting the presence of cancer, especially prostate cancer.
CC The polypeptides, polynucleotides and the antigen-presenting cells are
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein, and for inhibiting the development of cancer especially prostate
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC useful for stimulating an immune response, and for treating cancer. The
CC oligonucleotide is useful for detecting cancer. The present sequence is a
CC prostate specific polypeptide of the invention
XX
SQ Sequence 318 AA;
XX
Query Match 95.1%; Score 1577; DB 4; Length 318;
Best Local Similarity 98.7%; Pred. No. 5.9e-155;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 MVELMPFLILLIPFLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKE 60

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Db 1 MVELMPFLLILLPFLLYMAAPQIRKMLSSGVCSTVQLPKGVVVTGANTGICKETAKE 60
 QY 61 LAQGARVYLACRDVEKELVAKEIQTGGNOQVLRKLDLSDTKSIRAMAKGFAEEKH 120
 Db 61 LAQGARVYLACRDVEKELVAKEIQTGGNOQVLRKLDLSDTKSIRAFKGFALAEKH 120
 QY 121 LHWINNAGVMCPYSKTADGFEMHIGVNLGHFLTHLLLEKLSAPSRIVVSSLAH 180
 Db 121 LHWINNAGVMCPYSKTADGFEMHIGVNLGHFLTHLLLEKLSAPSRIVVSSLAH 180
 QY 181 HLGRIHFNHLOGEKRYNAGLAACHSKLANILFTQELARLKGSGVTTYSVHPGTVOSELY 240
 Db 181 HLGRIHFNHLOGEKRYNAGLAACHSKLANILFTQELARLKGSGVTTYSVHPGTVOSELY 240
 QY 241 RHSSFRMMWMLFSFFIKTPQOGAQTSLHCAITGELTSLGNHPSDCHVAVWSAQARNET 300
 Db 241 RHSSFRMMWMLFSFFIKTPQOGAQTSLHCAITGELTSLGNHPSDCHVAVWSAQARNET 300
 QY 301 IARLMDV 308
 Db 301 IARLMDV 308
 Db 301 IARLMDV 308
 RESULT 7
 AAB74812
 ID AAB74812 standard; protein, 318 AA.
 AC AAB74812;
 DT 14-JUN-2001 (first entry)
 DE Prostate tumour antigen predicated amino acid sequence for P509S.
 DE Prostate tumour antigen; prostate tumour; therapy; diagnosis;
 KM prostate cancer; immunogenic; cytostatic; vaccine.
 OS Homo sapiens.
 OS WO200125272-A2.
 PN 12-APR-2001.
 XX 04-OCT-2000; 2000WO-US027464.
 XX 04-OCT-1999; 99US-0157455P.
 XX (CORI-) CORIXA CORP.
 XX Xu J, Skeiky YAM, Reed SG, Cheever MA;
 PI WPI; 2001-245062/25.
 DR N-PSDB; AAH02742.
 XX Prostate specific protein and its encoding polynucleotide, useful for the
 PT treatment and diagnosis of prostate cancer.
 XX Claim 3; Page 220-221; 276pp; English.
 PS The present invention describes an isolated polypeptide (I) comprising at
 CC least an immunogenic portion of a prostate tumour antigen protein or its
 CC variant. (I) have cytostatic activity and can be used in vaccine
 CC production. (I), prostate tumour antigen polynucleotides, an antigen
 CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
 CC pharmaceutical composition containing (I) are useful for inhibiting the
 CC development of cancer in a patient. Antibodies specific for prostate
 CC specific proteins and oligonucleotides that hybridise to a polynucleotide
 CC that encodes a prostate specific protein are useful for detecting the
 CC presence or absence of a cancer or monitoring the progression the
 CC progression of a cancer, especially prostate cancer. AAH02422 to AAH2872,
 CC AAB74798 to AAB74821 and AAB74830 are sequences used in the
 CC exemplification of the present invention

SQ Sequence 318 AA;
 Query Match 95.1%; Score 1577; DB 4; Length 318;
 Best Local Similarity 98.7%; Pred. No. 5.9e-155;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MVELMPFLLILLPFLLYMAAPQIRKMLSSGVCSTVQLPKGVVVTGANTGICKETAKE 60
 Db 1 MVELMPFLLILLPFLLYMAAPQIRKMLSSGVCSTVQLPKGVVVTGANTGICKETAKE 60
 QY 61 LAQGARVYLACRDVEKELVAKEIQTGGNOQVLRKLDLSDTKSIRAMAKGFAEEKH 120
 Db 61 LAQGARVYLACRDVEKELVAKEIQTGGNOQVLRKLDLSDTKSIRAFKGFALAEKH 120
 QY 121 LHWINNAGVMCPYSKTADGFEMHIGVNLGHFLTHLLLEKLSAPSRIVVSSLAH 180
 Db 121 LHWINNAGVMCPYSKTADGFEMHIGVNLGHFLTHLLLEKLSAPSRIVVSSLAH 180
 QY 181 HLGRIHFNHLOGEKRYNAGLAACHSKLANILFTQELARLKGSGVTTYSVHPGTVOSELY 240
 Db 181 HLGRIHFNHLOGEKRYNAGLAACHSKLANILFTQELARLKGSGVTTYSVHPGTVOSELY 240
 QY 241 RHSSFRMMWMLFSFFIKTPQOGAQTSLHCAITGELTSLGNHPSDCHVAVWSAQARNET 300
 Db 241 RHSSFRMMWMLFSFFIKTPQOGAQTSLHCAITGELTSLGNHPSDCHVAVWSAQARNET 300
 QY 301 IARLMDV 308
 Db 301 IARLMDV 308
 Db 301 IARLMDV 308
 RESULT 8
 AAG99014
 ID AAG99014 standard; protein, 318 AA.
 AC AAG99014;
 DT 25-SEP-2001 (first entry)
 DE Human prostate-specific amino acid sequence P509S.
 DE Human prostate-specific amino acid sequence P509S.
 KM Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
 KM chromosome 22q11.2; prostate-specific protein; chromosome 1;
 KM prostate specific antigen; PSA.
 OS Homo sapiens.
 OS WO200134802-A2.
 PN 17-MAY-2001.
 XX 09-NOV-2000; 2000WO-US030904.
 XX 12-NOV-1999; 99US-00439313.
 XX 18-NOV-1999; 99US-00443686.
 XX (CORI-) CORIXA CORP.
 XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
 PI Kaios MD, Retter MW, Scolk JA, Day CH, Skeiky YAM, Wang A;
 DR WPI; 2001-308785/32.
 XX Isolated polypeptide comprising at least an immunogenic portion of a
 PT prostate-specific protein, useful in the diagnosis and therapy of
 PT prostate cancer.
 PS Claim 3; Page 234-235; 325pp; English.
 CC The present invention describes an isolated polypeptide (P1) comprising
 CC at least an immunogenic portion of a prostate-specific protein, or its
 CC variant. Also described are polynucleotides (N1) encoding (P1) and
 CC (N1) have cytostatic activity and can be used in vaccine production. The

CC polypeptides, nucleic acids and antibodies from the present invention are
 CC useful in the diagnosis and therapy of prostate cancer. Prostate specific
 CC genes P704P, P712P, P774P, P775P and B305D are located in a genomic
 CC region on chromosome 22q11.2 known as the Cat Eye Syndrome region.
 CC Prostate specific antigen (PSA) P501S was located on chromosome 1.
 CC AA84671 to AA85143 and AAG9800 to AAG9977 represent polynucleotide
 CC and polypeptide sequences used in the exemplification of the present
 CC invention

CC Sequence 318 AA;

Query Match 95.1%; Score 1577; DB 4; Length 318;
 Best Local Similarity 98.7%; Pred. No. 5.9e-155;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVELMPELLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKE 60
 DB 1 MVELMPELLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKE 60
 QY 61 LAQGARVYLACRVEKELVAKEIOTTGNOQVLRKLDLSDTKSIRAMAKGFAEEKH 120
 DB 61 LAQGARVYLACRVEKELVAKEIOTTGNOQVLRKLDLSDTKSIRAMAKGFAEEKH 120
 QY 121 LHVINNAGVMMCPYSKTADGPEMHTGVNHLGHFLTHLLLEKESASRIVNSSLAH 180
 DB 121 LHVINNAGVMMCPYSKTADGPEMHTGVNHLGHFLTHLLLEKESASRIVNSSLAH 180
 QY 181 HLGRIHFHNLQGEKFNAGLAICHSKLANILFTQELARLKSGGVTTYSVHGTVQSELY 240
 DB 181 HLGRIHFHNLQGEKFNAGLAICHSKLANILFTQELARLKSGGVTTYSVHGTVQSELY 240
 QY 241 RHSSFRMWMWLFSPFIKTPQOGAQRRLHCAITLSEGLISGNHFSDCHVAVWSAQAARNET 300
 DB 241 RHSSFRMWMWLFSPFIKTPQOGAQRRLHCAITLSEGLISGNHFSDCHVAVWSAQAARNET 300
 QY 301 IARLMDV 308
 DB 301 IARLMDV 308

RESULT 9

ID ABU71665 standard; protein; 318 AA.

XX ABU71665;
 XX 10-JUN-2003 (first entry)
 DE Prostate cancer associated protein #6.
 XX Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen; PSA;
 KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 XX PEMA.
 OS Homo sapiens.
 PN US2002192763-A1.
 PD 19-DEC-2002.
 PF 29-JUN-2001; 2001US-00895793.
 XX 04-OCT-1999; 99US-0157455P.
 PR 04-OCT-2000; 2000US-00679272.
 PR 28-MAR-2001; 2001US-00822827.
 XX (XUJ/) XU J.
 PA (DILL/) DILLON D. C.
 PA (MITC/) MITCHAM J. L.
 PA (HARL/) HARLOCKER S. L.
 PA (JIANG/) JIANG Y.
 PA (KALOS/) KALOS M. D.

PA (FANG/) FANGER G. R.
 PA (RETT/) RETTER M. W.
 PA (STOL/) STOLK J. A.
 PA (DAYC/) DAY C. H.
 PA (VEDV/) VEDVICK T. S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S. X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y. A. W.
 PA (HEPL/) HEPLER M. T.
 PA (HEND/) HENDERSON R. A.
 PA (HURA/) HURAL J.
 PA (MCNE/) MCNEILL P. D.
 PA (HOUG/) HOUGHTON R. L.
 PA (DEAS/) Y. DE BASSOLS C. V.
 PA (FOYT/) FOY T. M.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 Li SX, Wang A, Skeiky YAW, Hepler MT, Henderson RA, Hural J;
 Mcneill PD, Houghton RL, Y De Bassolcv, Foy TM;
 WPI; 2001-245062/25.

Prostate specific protein and its encoding polynucleotide, useful for the
 treatment and diagnosis of prostate cancer.

Example 1; SEQ ID NO 319; 85pp; English.

The invention describes a fusion protein comprising at least one amino
 acid sequence of immunogenic portions of any of the 3 sequences not
 defined in the specification, or sequences having at least 70 or 90 %
 sequence identity to any one of the 3 sequences defined in the USPTO web
 site, which is encoded by any of the 4 nucleotide sequences not defined
 in the specification. The fusion protein, composition and methods are
 useful for diagnosing, preventing and/or treating cancer, particularly
 prostate cancer. The proteins are useful as markers to indicate the
 presence or absence of cancer. This is the amino acid sequence of a
 prostate cancer therapy associated protein. Note: The sequence data for
 this patent did not form part of the printed specification, but was
 obtained in electronic format directly from the US patent office at
 seqdata.uspto.gov/sequence.html?docid=US20020192763

Sequence 318 AA;

Query Match 95.1%; Score 1577; DB 4; Length 318;
 Best Local Similarity 98.7%; Pred. No. 5.9e-155;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVELMPELLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKE 60
 DB 1 MVELMPELLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKE 60
 QY 61 LAQGARVYLACRVEKELVAKEIOTTGNOQVLRKLDLSDTKSIRAMAKGFAEEKH 120
 DB 61 LAQGARVYLACRVEKELVAKEIOTTGNOQVLRKLDLSDTKSIRAMAKGFAEEKH 120
 QY 121 LHVINNAGVMMCPYSKTADGPEMHTGVNHLGHFLTHLLLEKESASRIVNSSLAH 180
 DB 121 LHVINNAGVMMCPYSKTADGPEMHTGVNHLGHFLTHLLLEKESASRIVNSSLAH 180
 QY 181 HLGRIHFHNLQGEKFNAGLAICHSKLANILFTQELARLKSGGVTTYSVHGTVQSELY 240
 DB 181 HLGRIHFHNLQGEKFNAGLAICHSKLANILFTQELARLKSGGVTTYSVHGTVQSELY 240
 QY 241 RHSSFRMWMWLFSPFIKTPQOGAQRRLHCAITLSEGLISGNHFSDCHVAVWSAQAARNET 300
 DB 241 RHSSFRMWMWLFSPFIKTPQOGAQRRLHCAITLSEGLISGNHFSDCHVAVWSAQAARNET 300
 QY 301 IARLMDV 308
 DB 301 IARLMDV 308

RESULT 10
ABG96558
ID ABG96558 standard; protein; 318 AA.
AC ABG96558;
XX
XX 12-DEC-2002 (first entry)
DE Human short chain dehydrogenase family member CGI-82.
XX
KM Short chain dehydrogenase; SDR; human; antimetabolic; pesticide;
KM herbicide; DHR deficiency; phenylketonuria; galactosaemia III;
KM dienoil CoA reductase deficiency; adrenal hyperplasia; ovarian cancer;
KM adrenogenital syndrome; mineralocorticoid excess syndrome; breast cancer;
KM male pseudohemaphroditism; Zellweger syndrome; Down's syndrome;
KM polycystic kidney disease; Alzheimer's disease; retinitis pigmentosa;
KM retinitis punctata albescens; arterial hypertension; follicular lymphoma;
KM hepatocarcinogenesis; fungicide; antibiotic.
XX
OS Homo sapiens.
XX
XX WO200212544-A2.
XX
XX 14-FEB-2002.
XX
XX 07-AUG-2001; 2001WO-EP009140.
XX
XX 07-AUG-2000; 2000US-0223436P.
XX
XX (BION-) BIONETWORKS GMBH.
XX
XX Wilckens T;
XX
XX WPI; 2002-241770/29.
XX
XX Identifying or verifying members of the short chain dehydrogenase (SDR)
XX family, useful for novel drug development (e.g. for the development of
XX antimetabolic, pesticides or herbicides), by employing an algorithm using
XX core SDR motifs.
XX
XX Disclosure; Fig 4; 16pp; English.
XX
XX The invention relates to identifying or verifying members of the short
XX chain dehydrogenase (SDR) family comprises employing an algorithm using
XX core SDR motifs (MT1-MT4 and MVI, MY2 given in the specification) for
XX searching members of the SDR family. Also included are a member of the
XX SDR family identified with the method above, a method for providing
XX modulators for members of the SDR family, a method for evaluation of lead
XX -candidates for possible modulators of a member of the SDR family and a
XX method for detecting clinically relevant polymorphisms or single
XX nucleotide polymorphisms. The method is useful for screening SDR
XX sequences and modulators of the SDR family. The method is especially
XX useful as a platform for novel drug development. The SDRs can serve for
XX the development of e.g. antimetabolic, pesticides or herbicides. The
XX modulators may be especially useful for the prophylaxis, treatment of/and
XX diagnosis of diseases (e.g. DHR deficiency, phenylketonuria, dienoil CoA
XX reductase deficiency, galactosaemia III, adrenal hyperplasia,
XX adrenogenital syndrome, mineralocorticoid excess syndrome, ovarian cancer,
XX breast cancer, male pseudohemaphroditism, Zellweger syndrome, polycystic
XX kidney disease, Alzheimer's disease, retinitis punctata albescens,
XX retinitis pigmentosa, Down's syndrome, arterial hypertension, follicular
XX lymphoma and hepatocarcinogenesis) particularly as a fungicide or
XX antibiotic. The present sequence is one of 39 human SDR family members
XX identified by the method of the invention
XX
XX Sequence 318 AA;
SQ

Query Match 95.1%; Score 1577; DB 5; Length 318;
Best Local Similarity 98.7%; Pred. No. 5,9e-155;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 MVELMFPULLLLPLLYMAAPQIRKMLSSGVCSTVQLPKGVVVVGANTGIGETAKE 60

DB 1 MVELMFPULLLLPLLYMAAPQIRKMLSSGVCSTVQLPKGVVVVGANTGIGETAKE 60
QY 61 LAORGARVYIACRDVEKSELVAKKEIOTTGNQOVVRKLD;SDTKSIRAMAKGFABEKH 120
DB 61 LAORGARVYIACRDVEKSELVAKKEIOTTGNQOVVRKLD;SDTKSIRAPAKGFLABEKH 120
QY 121 LHWINNAGVMMCPYSKTADGFEHAIQVNHLLGHFLLTHLLLEKESAPSRIVNVSSLAH 180
DB 121 LHWINNAGVMMCPYSKTADGFEHAIQVNHLLGHFLLTHLLLEKESAPSRIVNVSSLAH 180
QY 181 HLGRIHFHNLQGEKRYNGLACYSKLANILFTQELARIKSGVTTYSVHPGTQOSLIV 240
DB 181 HLGRIHFHNLQGEKRYNGLACYSKLANILFTQELARIKSGVTTYSVHPGTQOSLIV 240
QY 241 RHSSFMKMMWMLFSEFIKTPQOGAOTRLHCAITGELIILSGNHPSDCHVAMVSAQARNET 300
DB 241 RHSSFMKMMWMLFSEFIKTPQOGAOTSLHCAITGELIILSGNHPSDCHVAMVSAQARNET 300
QY 301 IARRLMDV 308
DB 301 IARRLMDV 308
DB 301 IARRLMDV 308

RESULT 11
ABB95234
ID ABB95234 standard; protein; 318 AA.
XX
XX ABB95234;
XX
XX 19-JUL-2002 (first entry)
XX
XX Human P509S protein SEQ ID NO 339.
XX
XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy.
XX
XX Homo sapiens.
XX
XX US2002022248-A1.
XX
XX 21-FEB-2002.
XX
XX 12-JAN-2001; 2001US-00759143.
XX
XX 25-FEB-1997; 97US-008606099.
XX
XX 01-AUG-1997; 97US-00904804.
XX
XX 10-FEB-1998; 98US-00020956.
XX
XX 25-FEB-1998; 98US-00030607.
XX
XX 14-JUL-1998; 98US-00115453.
XX
XX 23-SEP-1998; 98US-00159812.
XX
XX 15-JAN-1999; 99US-00232149.
XX
XX 09-APR-1999; 99US-00289946.
XX
XX 13-JUL-1999; 99US-00352616.
XX
XX 12-NOV-1999; 99US-00439313.
XX
XX 18-NOV-1999; 99US-00443686.
XX
XX 14-JAN-2000; 2000US-00483672.
XX
XX 27-MAR-2000; 2000US-00536857.
XX
XX 09-MAY-2000; 2000US-00568100.
XX
XX 12-MAY-2000; 2000US-00570737.
XX
XX 13-JUN-2000; 2000US-00593793.
XX
XX 27-JUN-2000; 2000US-00605783.
XX
XX 10-AUG-2000; 2000US-00636215.
XX
XX 29-AUG-2000; 2000US-00651236.
XX
XX 06-SEP-2000; 2000US-00657279.
XX
XX 02-OCT-2000; 2000US-00679426.
XX
XX 10-OCT-2000; 2000US-00685166.
XX
XX (XU05/) XU J.
XX
XX (DILL/) DILLON D C.
XX
XX (MITC/) MITCHAM J L.
XX
XX (HARL/) HARLOCKER S L.
XX
XX (JIAN/) JIANG Y.

PA (KALO/) KALOS M. D.
 PA (FANG/) FANGER G. R.
 PA (RETT/) RETTER M. W.
 PA (STOL/) STOLK J. A.
 PA (DAYC/) DAY C. H.
 PA (VEDV/) VEDVICK T. S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S. X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y. A. W.
 PA (HEPL/) HEPLER W. T.
 PA (HEND/) HENDERSON R. A.
 XX
 PI Xu J., Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX
 DR WPI; 2002-255649/30.
 XX
 PT New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer.
 PS
 PS Claim 2; SEQ ID NO 339; 87bp; English.
 XX
 CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a
 CC protein described in the invention
 XX
 SQ Sequence 318 AA;
 Query Match 95.1%; Score 1577; DB 5; Length 318;
 Best Local Similarity 98.7%; Pred. No. 5.9e-155;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MVELMPFLLLLPFLLYMAAPQIRKMLSSGCVCTSTVQLPGKVVVVTGANTGIGKETAKE 60
 DB 1 MVELMPFLLLLPFLLYMAAPQIRKMLSSGCVCTSTVQLPGKVVVVTGANTGIGKETAKE 60
 QY 61 LAQRGARVYLACRDVEKGEIVAKEIOTTGNQOVLVRKLDLSDTKSIRAWAKGFKAEEKH 120
 DB 61 LAQRGARVYLACRDVEKGEIVAKEIOTTGNQOVLVRKLDLSDTKSIRAFAGFLAEEKH 120
 QY 121 LHVAINNAGVMMCPYSKTADGFEMHIGVNHGFLTLTHLLEKXESAPSRIVNVSSLAH 180
 DB 121 LHVAINNAGVMMCPYSKTADGFEMHIGVNHGFLTLTHLLEKXESAPSRIVNVSSLAH 180
 QY 181 HLGRIHFHNLQGEKFFNAGLAYCHSKLANILFTQELARLKSGGVTTYSVHPGTVOSELY 240
 DB 181 HLGRIHFHNLQGEKFFNAGLAYCHSKLANILFTQELARLKSGGVTTYSVHPGTVOSELY 240
 QY 241 RHSSFMKMMWMLFSFFIKTPQOQAQTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300
 DB 241 RHSSFMKMMWMLFSFFIKTPQOQAQTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300
 QY 301 IARRLMDV 308
 DB 301 IARRLMDV 308
 RESULT 12
 ID ABR54346 standard; protein; 318 AA.
 XX
 AC ABR54346;
 XX
 DT 28-AUG-2003 (first entry)
 XX
 DE Prostate tumour specific protein sequence SEQ ID 339.
 XX
 KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
 KW immune response; prostate cancer.

XX
 OS Homo sapiens.
 XX
 PN WO200289747-A2.
 XX
 XX
 PD 14-NOV-2002.
 XX
 PF 09-MAY-2002; 2002WO-US014753.
 XX
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J., Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
 PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
 PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
 PI McNeill PD, Houghton RL, Vinals Y De Baasolac, Foy TM, Watanabe Y;
 PI Deng T;
 XX
 DR WPI; 2003-167130/16.
 XX
 PT New prostate-specific proteins and genes, useful in gene therapy,
 PT particularly for stimulating an immune response in a patient, or treating
 PT prostate cancer in a patient, as well as for diagnosing prostate cancer
 PT in a patient.
 PS
 PS Example 1; Page 402-403; 691bp; English.
 XX
 CC The present invention relates to novel prostate-specific proteins (PSP)
 CC and their coding sequences. The PSPs and their coding sequences are
 CC useful for stimulating an immune response in a patient, or for treating
 CC prostate cancer in a patient and for determining, detecting or diagnosing
 CC the presence of a cancer in a patient. The present sequence was used to
 CC illustrate the invention
 XX
 SQ Sequence 318 AA;
 Query Match 95.1%; Score 1577; DB 6; Length 318;
 Best Local Similarity 98.7%; Pred. No. 5.9e-155;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MVELMPFLLLLPFLLYMAAPQIRKMLSSGCVCTSTVQLPGKVVVVTGANTGIGKETAKE 60
 DB 1 MVELMPFLLLLPFLLYMAAPQIRKMLSSGCVCTSTVQLPGKVVVVTGANTGIGKETAKE 60
 QY 61 LAQRGARVYLACRDVEKGEIVAKEIOTTGNQOVLVRKLDLSDTKSIRAWAKGFKAEEKH 120
 DB 61 LAQRGARVYLACRDVEKGEIVAKEIOTTGNQOVLVRKLDLSDTKSIRAFAGFLAEEKH 120
 QY 121 LHVAINNAGVMMCPYSKTADGFEMHIGVNHGFLTLTHLLEKXESAPSRIVNVSSLAH 180
 DB 121 LHVAINNAGVMMCPYSKTADGFEMHIGVNHGFLTLTHLLEKXESAPSRIVNVSSLAH 180
 QY 181 HLGRIHFHNLQGEKFFNAGLAYCHSKLANILFTQELARLKSGGVTTYSVHPGTVOSELY 240
 DB 181 HLGRIHFHNLQGEKFFNAGLAYCHSKLANILFTQELARLKSGGVTTYSVHPGTVOSELY 240
 QY 241 RHSSFMKMMWMLFSFFIKTPQOQAQTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300
 DB 241 RHSSFMKMMWMLFSFFIKTPQOQAQTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300
 QY 301 IARRLMDV 308
 DB 301 IARRLMDV 308
 RESULT 13
 ID ADB75403 standard; protein; 318 AA.
 XX
 AC ADB75403;
 AC ADB75403;

XX 04-DEC-2003 (first entry)
 DT
 XX Prostate cancer marker protein.
 DE
 XX Prostate; cancer; cytostatic; gene therapy; marker.
 KW
 XX Homo sapiens.
 OS
 XX WO2003009614-A2.
 PN
 XX 06-FEB-2003.
 PD
 XX 25-JUL-2002; 2002WO-US023913.
 PF
 XX 25-JUL-2001; 2001US-0307982P.
 PR 22-AUG-2001; 2001US-0314356P.
 PR 25-SEP-2001; 2001US-0325020P.
 PR 12-DEC-2001; 2001US-0341746P.
 PR 05-MAR-2002; 2002US-0362158P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Schlegel R, Monahan JF, Endege WO, Gannavarapu M, Gorbacheva B,
 PI Hoerish S, Kamatkar S, Wonsey AW, Glatk K, Zhao X, Anderson D,
 XX
 DR WPI; 2003-248033/24.
 XX
 PT New nucleic acid molecule, useful for diagnosing or treating prostate
 PT cancer.
 XX
 PS Claim 4; SEQ ID NO 227; 99pp; English.
 XX
 CC The invention relates to newly discovered cancer markers associated with
 CC the cancerous state of prostate cells. Also disclosed is a method of
 CC assessing whether a patient is afflicted with prostate cancer. The method
 CC of the invention involves assessing whether a patient is afflicted with
 CC prostate cancer by comparing the level of expression of a marker in a
 CC patient sample and the normal level of expression of the marker in the
 CC control non-prostate cancer sample, where a significant increase in the
 CC level of expression of the marker in the patient sample and the normal
 CC level indicates that the patient is afflicted with prostate cancer.
 CC Nucleic acids of the invention are useful for diagnosing or treating
 CC prostate cancer, and may be useful in gene therapy. Sequences given in
 CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 318 AA;
 Query Match 95.1%; Score 1577; DB 7; Length 318;
 Best Local Similarity 98.7%; Pred. No. 5,9e-155;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MEIWPFLILLPLFLVMAAPQIRKMSGGVCTSTVQPGVVVVTGANTGIGETAKE 60
 DB 1 MEIWPFLILLPLFLVMAAPQIRKMSGGVCTSTVQPGVVVVTGANTGIGETAKE 60
 QY 61 LAQRGARVYLACRDVEKELVAKEIQTITGNOQVLRKIDISDTYSIRAMAKGFABEKH 120
 DB 61 LAQRGARVYLACRDVEKELVAKEIQTITGNOQVLRKIDISDTYSIRAMAKGFABEKH 120
 QY 121 LEWYINNAQVMCPYSKTDGFEHMGVNHGHFLTHLLEKLESAPSRIVNSSLAH 180
 DB 121 LEWYINNAQVMCPYSKTDGFEHMGVNHGHFLTHLLEKLESAPSRIVNSSLAH 180
 QY 181 HLGRIHFHNLQGEKFNAGLAYCHSKLANILFTQELARRLKSGVYTVSHPGTVQSELY 240
 DB 181 HLGRIHFHNLQGEKFNAGLAYCHSKLANILFTQELARRLKSGVYTVSHPGTVQSELY 240
 QY 241 RHSSFRMWMWLFSPFIKTPOQGAQTRLCALTEGIELISGNHPSCHYAWVSAQARNET 300
 DB 241 RHSSFRMWMWLFSPFIKTPOQGAQTRLCALTEGIELISGNHPSCHYAWVSAQARNET 300

DB 241 RHSSFRMWMWLFSPFIKTPOQGAQTRLCALTEGIELISGNHPSCHYAWVSAQARNET 300
 QY 301 IARRLMDV 308
 DB 301 IARRLMDV 308
 RESULT 14
 ADB13789
 ID ADB13789 standard; protein; 318 AA.
 XX
 AC ADB13789;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human prostate specific protein P509S.
 XX
 KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
 KW cell therapy; vaccine; T-cell epitope;
 KW class I major histocompatibility complex allele; MHC; prostate cancer;
 KW tumour; antigen presenting cell.
 XX
 OS Homo sapiens.
 XX
 PN US2003185830-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 12-NOV-2002; 2002US-00294025.
 XX
 PR 25-FEB-1997; 97US-00806099.
 PR 01-AUG-1997; 97US-00904804.
 PR 09-FEB-1998; 98US-00020956.
 PR 25-FEB-1998; 98US-00030607.
 PR 14-JUL-1998; 98US-00115453.
 PR 23-SEP-1998; 98US-00159812.
 PR 15-JAN-1999; 99US-00232149.
 PR 09-APR-1999; 99US-00288946.
 PR 13-JUL-1999; 99US-00352616.
 PR 12-NOV-1999; 99US-00439312.
 PR 18-NOV-1999; 99US-00443686.
 PR 14-JAN-2000; 2000US-00483672.
 PR 27-MAR-2000; 2000US-00536857.
 PR 09-MAY-2000; 2000US-00568100.
 PR 12-MAY-2000; 2000US-00570737.
 PR 13-JUN-2000; 2000US-00593793.
 PR 27-JUN-2000; 2000US-00605783.
 PR 09-AUG-2000; 2000US-00636215.
 PR 29-AUG-2000; 2000US-00651236.
 PR 06-SEP-2000; 2000US-00657279.
 PR 02-OCT-2000; 2000US-00679426.
 PR 10-OCT-2000; 2000US-00685166.
 PR 09-NOV-2000; 2000US-00709729.
 PR 12-JAN-2001; 2001US-00759143.
 PR 09-FEB-2001; 2001US-00780669.
 PR 09-MAY-2001; 2001US-00852911.
 PR 29-JUN-2001; 2001US-00895814.
 PR 10-DEC-2001; 2001US-00012896.
 PR 09-MAY-2002; 2002US-00144678.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 PI Xu J, Stolk JA, Kalos MD;
 XX
 DR WPI; 2003-756193/71.
 XX
 DR N-PSDB; ADB13782.
 XX
 PT New isolated polypeptide for use in a vaccine for stimulating an immune
 PT response, or for treating or diagnosis cancer, preferably prostate
 PT cancer.
 XX
 PS Example 1; Page: 10pp; English.
 XX

XX
SQ Sequence 318 AA;

Query Match 95.1%; Score 1577; DB 7; Length 318;
Best Local Similarity 98.7%; Pred. No. 5.9e-155;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY	1	MVELMPFLLLLLLPFLLYMAAPQIRKRLSSGVCSTVQLPGKVVVVTGANTGIGKETAKE	60
DB	1	MVELMPFLLLLLLPFLLYMAAPQIRKRLSSGVCSTVQLPGKVVVVTGANTGIGKETAKE	60
QY	61	LAQGARVYLACRDVEKGEIVAKEIOTTGNOQVLYAKLDLSDTKSIRANAKGFKAEKE	120
DB	61	LAQGARVYLACRDVEKGEIVAKEIOTTGNOQVLYAKLDLSDTKSIRAFKGFLEBEK	120
QY	121	LHWVWNNAGVMMCPYSKTADGFEMHIGVNHGHFLTLHLLEKLEKESAPSRIVVSSLAH	180
DB	121	LHVLINNAGVMMCPYSKTADGFEMHIGVNHGHFLTLHLLEKLEKESAPSRIVVSSLAH	180
QY	181	HLGRHHPNLOGEKEFYNAGLAYCHSKLANILFTQELARLKGSGVTTSVHPGTVOSELV	240
DB	181	HLGRHHPNLOGEKEFYNAGLAYCHSKLANILFTQELARLKGSGVTTSVHPGTVOSELV	240
QY	241	RHSSFMRRMMWLFSFFIKTPOQGAQTRLHCLTEGLEILSGNHPSDCHVAMVSAQARNET	300
DB	241	RHSSFMRRMMWLFSFFIKTPOQGAQTSIHCLTEGLEILSGNHPSDCHVAMVSAQARNET	300
QY	301	IARRLMDV 308	
DB	301	IARRLMDV 308	

Search completed: October 13, 2004, 18:11:49
Job time : 161 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 18:13:15 ; Search time 131 Seconds

(without alignments)
778.380 Million cell updates/sec

Title: US-10-021-002-2

Perfect score: 1559
Sequence: 1 MWELMFPLLLLPFLLYMA.....RNFTIRRLMDVITWQASQ 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 1356558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1559	100.0	316	13	US-10-021-002-2
2	1577	95.1	318	9	US-09-759-143-339
3	1577	95.1	318	9	US-09-780-669-339
4	1577	95.1	318	9	US-09-822-827-339
5	1577	95.1	318	9	US-09-895-793-339
6	1577	95.1	318	9	US-09-895-814-339
7	1577	95.1	318	13	US-10-012-896-339
8	1577	95.1	318	14	US-10-010-940-339
9	1577	95.1	318	14	US-10-205-823-227
10	1577	95.1	318	14	US-10-144-678A-339
11	1577	95.1	318	14	US-10-294-025-339
12	1577	95.1	318	15	US-10-080-334-98
13	1577	95.1	318	16	US-10-408-765A-3006
14	1577	95.1	333	14	US-10-131-410-147

15	1577	95.1	335	14	US-10-131-410-198	Sequence 198, App
16	1573	91.8	318	15	US-10-080-334-97	Sequence 97, App1
17	1347.5	81.2	316	15	US-10-080-334-99	Sequence 99, App1
18	1347.5	81.2	316	15	US-10-074-978A-424	Sequence 424, App
19	1345.5	81.1	353	15	US-10-074-978A-425	Sequence 425, App
20	1291	77.8	293	15	US-10-074-978A-422	Sequence 422, App
21	1279	77.1	293	15	US-10-074-978A-423	Sequence 423, App
22	1130	68.1	316	14	US-10-094-749-1760	Sequence 1760, App
23	1129	68.1	316	14	US-10-286-506-1	Sequence 1, App1
24	1059	63.8	316	15	US-10-080-334-95	Sequence 95, App1
25	1020	61.5	278	15	US-10-080-334-92	Sequence 2, App1
26	1005	60.6	304	15	US-10-080-334-96	Sequence 96, App1
27	806	48.6	246	14	US-10-168-374-18	Sequence 18, App1
28	705.5	42.5	331	10	US-09-946-374-116	Sequence 116, App
29	705.5	42.5	331	14	US-10-006-856A-116	Sequence 116, App
30	705.5	42.5	331	14	US-10-006-818A-116	Sequence 116, App
31	705.5	42.5	331	14	US-10-006-885A-116	Sequence 116, App
32	705.5	42.5	331	14	US-10-013-907A-116	Sequence 116, App
33	705.5	42.5	331	14	US-10-015-499A-116	Sequence 116, App
34	705.5	42.5	331	14	US-10-015-499A-116	Sequence 116, App
35	705.5	42.5	331	14	US-10-015-869A-116	Sequence 116, App
36	705.5	42.5	331	14	US-10-012-121A-116	Sequence 116, App
37	705.5	42.5	331	14	US-10-006-116A-116	Sequence 116, App
38	705.5	42.5	331	14	US-10-006-117A-116	Sequence 116, App
39	705.5	42.5	331	14	US-10-017-527A-116	Sequence 116, App
40	705.5	42.5	331	14	US-10-013-913A-116	Sequence 116, App
41	705.5	42.5	331	14	US-10-007-194A-116	Sequence 116, App
42	705.5	42.5	331	14	US-10-013-430A-116	Sequence 116, App
43	705.5	42.5	331	14	US-10-011-671A-116	Sequence 116, App
44	705.5	42.5	331	14	US-10-012-755A-116	Sequence 116, App
45	705.5	42.5	331	14	US-10-015-386A-116	Sequence 116, App

ALIGNMENTS

RESULT 1
US-10-021-002-2
Sequence 2, Application US/10021002
Publication No. US20020150578A1
GENERAL INFORMATION:
APPLICANT: He, et al.
TITLE OF INVENTION: Human Prostatic Specific Reductase
FILE REFERENCE: PFI50D2
CURRENT APPLICATION NUMBER: US/10/021,002
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: PCT/US95/01827
PRIOR FILING DATE: 1995-01-20
PRIOR APPLICATION NUMBER: 08/464,400
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 09/123,386
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 316
TYPE: PRT
ORGANISM: human
US-10-021-002-2
Query Match 100.0% Score 1659; DB 13; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWELMFPLLLLPFLLYMAADPIRKLSSGVCTSTVQLPGKVVVVTGANTGIGETAKE 60
1 MWELMFPLLLLPFLLYMAAPQIRKLSSGVCTSTVQLPGKVVVVTGANTGIGETAKE 60
DB 1 LAQRGRVYIACDVVKGEIVAKETIOTTGNOQVLRKLDSDTSIRAMAGFAKEEG 120
61 LAQRGRVYIACDVVKGEIVAKETIOTTGNOQVLRKLDSDTSIRAMAGFAKEEG 120
DB 61 LAQRGRVYIACDVVKGEIVAKETIOTTGNOQVLRKLDSDTSIRAMAGFAKEEG 120
121 LHWINNAGVMCPYSKTADEGEMHIGVNLGHFLTLLEKLEKESAPSRIVNSSLAH 180

Db 121 LHWINNAGVMMCPYSTADGFEMHIGVNHGHLTHLLEKLSAPSRIVNSSLAH 180
Qy 181 HLGRIHFNHIOGEKFNAGIAYCHSKLANILFTQELARRLKSGVTTYVHPGTVOSELY 240
Db 181 HLGRIHFNHIOGEKFNAGIAYCHSKLANILFTQELARRLKSGVTTYVHPGTVOSELY 240
Qy 241 RHSSFRMWWWLFSFFIKTPQOGAOTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300
Db 241 RHSSFRMWWWLFSFFIKTPQOGAOTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300
Qy 301 IARLMDVITVCNASQ 316
Db 301 IARLMDVITVCNASQ 316

RESULT 2
US-09-759-143-339
; Sequence 339, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-759-143-339

Query Match 95.1%; Score 1577; DB 9; Length 318;
Best Local Similarity 98.7%; Pred. No. 1.2e-143;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MVELMPFLLLLPFLLYMAAPQIRKMLSSGVCTSTVQJPGKVVVVTGANTGIGKETAKE 60
Db 1 MVELMPFLLLLPFLLYMAAPQIRKMLSSGVCTSTVQJPGKVVVVTGANTGIGKETAKE 60
Qy 61 LAORGARVYLACDVEKGEIVAKEIOTTGNQOVLRKLDLSTKSIIRAKGFKAEEKH 120
Db 61 LAORGARVYLACDVEKGEIVAKEIOTTGNQOVLRKLDLSTKSIIRAKGFKAEEKH 120
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Db 121 LHWINNAGVMMCPYSTADGFEMHIGVNHGHLTHLLEKLSAPSRIVNSSLAH 180
Qy 181 HLGRIHFNHIOGEKFNAGIAYCHSKLANILFTQELARRLKSGVTTYVHPGTVOSELY 240
Db 181 HLGRIHFNHIOGEKFNAGIAYCHSKLANILFTQELARRLKSGVTTYVHPGTVOSELY 240
Qy 241 RHSSFRMWWWLFSFFIKTPQOGAOTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300
Db 241 RHSSFRMWWWLFSFFIKTPQOGAOTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300

Db 241 RHSSFRMWWWLFSFFIKTPQOGAOTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300
Qy 301 IARLMDV 308
Db 301 IARLMDV 308

RESULT 3
US-09-780-669-339
; Sequence 339, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurel, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-780-669-339

Query Match 95.1%; Score 1577; DB 9; Length 318;
Best Local Similarity 98.7%; Pred. No. 1.2e-143;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MVELMPFLLLLPFLLYMAAPQIRKMLSSGVCTSTVQJPGKVVVVTGANTGIGKETAKE 60
Db 1 MVELMPFLLLLPFLLYMAAPQIRKMLSSGVCTSTVQJPGKVVVVTGANTGIGKETAKE 60
Qy 61 LAORGARVYLACDVEKGEIVAKEIOTTGNQOVLRKLDLSTKSIIRAKGFKAEEKH 120
Db 61 LAORGARVYLACDVEKGEIVAKEIOTTGNQOVLRKLDLSTKSIIRAKGFKAEEKH 120
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Db 121 LHWINNAGVMMCPYSTADGFEMHIGVNHGHLTHLLEKLSAPSRIVNSSLAH 180
Qy 181 HLGRIHFNHIOGEKFNAGIAYCHSKLANILFTQELARRLKSGVTTYVHPGTVOSELY 240
Db 181 HLGRIHFNHIOGEKFNAGIAYCHSKLANILFTQELARRLKSGVTTYVHPGTVOSELY 240
Qy 241 RHSSFRMWWWLFSFFIKTPQOGAOTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300
Db 241 RHSSFRMWWWLFSFFIKTPQOGAOTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300
Qy 301 IARLMDV 308
Db 301 IARLMDV 308

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RESULT 4
US-09-822-827-339
; Sequence 339, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-822-827-339

Query Match          95.1%; Score 1577; DB 9; Length 318;
Best Local Similarity 98.7%; Pred. No. 1.2e-143;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MWELMPFLLLLLPFLLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGKETAKE 60
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QY 61 LAORGARYYLAACRDVEKGEIVAKETQTTGNQOVYVRKLDSDTKSIRAPAKGFKAEEKH 120
DB 61 LAORGARYYLAACRDVEKGEIVAKETQTTGNQOVYVRKLDSDTKSIRAPAKGFKAEEKH 120
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DB 121 LHWINNAGVMMCPYKSTADGFEHMGVNHGFLTHLLLEKLESAPSRIVNVSSLAH 180
QY 181 HLGRIHFHNLQGEKRYNAGLAYCHSKLANILFTQSLARLKGSGVTTYSVHPGTVOSELV 240
DB 181 HLGRIHFHNLQGEKRYNAGLAYCHSKLANILFTQSLARLKGSGVTTYSVHPGTVOSELV 240
QY 241 RHSSFFRMWMLFSPFIKTPQGAQOTRLHCALTEGLEILSGNHPSDCHVAMVSAQARNET 300
DB 241 RHSSFFRMWMLFSPFIKTPQGAQOTRLHCALTEGLEILSGNHPSDCHVAMVSAQARNET 300
QY 301 IARRLMDV 308
DB 301 IARRLMDV 308

RESULT 5
US-09-895-793-339
; Sequence 339, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuguu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
```

```
; APPLICANT: Vinals de Baesols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-895-793-339

Query Match          95.1%; Score 1577; DB 9; Length 318;
Best Local Similarity 98.7%; Pred. No. 1.2e-143;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MWELMPFLLLLLPFLLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGKETAKE 60
DB 1 MWELMPFLLLLLPFLLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGKETAKE 60
QY 61 LAORGARYYLAACRDVEKGEIVAKETQTTGNQOVYVRKLDSDTKSIRAPAKGFKAEEKH 120
DB 61 LAORGARYYLAACRDVEKGEIVAKETQTTGNQOVYVRKLDSDTKSIRAPAKGFKAEEKH 120
QY 121 LHWINNAGVMMCPYKSTADGFEHMGVNHGFLTHLLLEKLESAPSRIVNVSSLAH 180
DB 121 LHWINNAGVMMCPYKSTADGFEHMGVNHGFLTHLLLEKLESAPSRIVNVSSLAH 180
QY 181 HLGRIHFHNLQGEKRYNAGLAYCHSKLANILFTQSLARLKGSGVTTYSVHPGTVOSELV 240
DB 181 HLGRIHFHNLQGEKRYNAGLAYCHSKLANILFTQSLARLKGSGVTTYSVHPGTVOSELV 240
QY 241 RHSSFFRMWMLFSPFIKTPQGAQOTRLHCALTEGLEILSGNHPSDCHVAMVSAQARNET 300
DB 241 RHSSFFRMWMLFSPFIKTPQGAQOTRLHCALTEGLEILSGNHPSDCHVAMVSAQARNET 300
QY 301 IARRLMDV 308
DB 301 IARRLMDV 308

RESULT 6
US-09-895-814-339
; Sequence 339, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuguu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Baesols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,614
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 318
TYPE: PR1
ORGANISM: Homo sapien
US-09-895-814-339

Query Match 95.1%; Score 1577; DB 9; Length 318;
Best Local Similarity 98.7%; Pred. No. 1,2e-143;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVELMPFLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVGANTGIGKETAKE 60
DB 1 MVELMPFLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVGANTGIGKETAKE 60
QY 61 LAORGARVYLA CRDVEKGEIVAKEIOTTGNOQVLVRKLDLSDTKSIRAWAKGFKAEEKH 120
DB 61 LAORGARVYLA CRDVEKGEIVAKEIOTTGNOQVLVRKLDLSDTKSIRAFKGFLEEKH 120
QY 121 LHWVNNAGVMMCPYKSTADGFEMHIGVNHGFLTHLLLEKLSKESAPSRIVNVSSLAH 180
DB 121 LHWVNNAGVMMCPYKSTADGFEMHIGVNHGFLTHLLLEKLSKESAPSRIVNVSSLAH 180
QY 181 HLGRIHFHNLQGEKFNAGLA YCHSKLANILFTQELARRLKGSGVTTYSHPGTVOSELY 240
DB 181 HLGRIHFHNLQGEKFNAGLA YCHSKLANILFTQELARRLKGSGVTTYSHPGTVOSELY 240
QY 241 RHSSFKRMWMLFSPFIKTPQOGAQTRLHCAITBGLFISGNHFSDCHVAVWSAQARNET 300
DB 241 RHSSFKRMWMLFSPFIKTPQOGAQTSLHCALTEGLIISGNHFSCHVAVWSAQARNET 300
QY 301 IARRLMDV 308
DB 301 IARRLMDV 308

RESULT 7

US-10-012-896-339
Sequence 339, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugui
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Solik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlotia
APPLICANT: Roy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshinhiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27

CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 318
TYPE: PR1
ORGANISM: Homo sapiens
US-10-012-896-339

Query Match 95.1%; Score 1577; DB 13; Length 318;
Best Local Similarity 98.7%; Pred. No. 1,2e-143;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVELMPFLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVGANTGIGKETAKE 60
DB 1 MVELMPFLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVGANTGIGKETAKE 60
QY 61 LAORGARVYLA CRDVEKGEIVAKEIOTTGNOQVLVRKLDLSDTKSIRAWAKGFKAEEKH 120
DB 61 LAORGARVYLA CRDVEKGEIVAKEIOTTGNOQVLVRKLDLSDTKSIRAFKGFLEEKH 120
QY 121 LHWVNNAGVMMCPYKSTADGFEMHIGVNHGFLTHLLLEKLSKESAPSRIVNVSSLAH 180
DB 121 LHWVNNAGVMMCPYKSTADGFEMHIGVNHGFLTHLLLEKLSKESAPSRIVNVSSLAH 180
QY 181 HLGRIHFHNLQGEKFNAGLA YCHSKLANILFTQELARRLKGSGVTTYSHPGTVOSELY 240
DB 181 HLGRIHFHNLQGEKFNAGLA YCHSKLANILFTQELARRLKGSGVTTYSHPGTVOSELY 240
QY 241 RHSSFKRMWMLFSPFIKTPQOGAQTRLHCAITBGLFISGNHFSDCHVAVWSAQARNET 300
DB 241 RHSSFKRMWMLFSPFIKTPQOGAQTSLHCALTEGLIISGNHFSCHVAVWSAQARNET 300
QY 301 IARRLMDV 308
DB 301 IARRLMDV 308

RESULT 8

US-10-010-940-339
Sequence 339, Application US/10010940
Publication No. US20030088062A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solik, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 318
TYPE: PR1
ORGANISM: Homo sapien
US-10-010-940-339

Query Match 95.1%; Score 1577; DB 14; Length 318;
Best Local Similarity 98.7%; Pred. No. 1,2e-143;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVELMPFLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVGANTGIGKETAKE 60

Db 1 MVELMPFLLLLPFLLYMAAPDIRKMLSSGVCSTSVQIPGKVVVVTGANTGIGKETAKE 60

Qy 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAKGFLAEK 120

Db 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAKGFLAEK 120

Qy 121 LHWINNAGVMMCPYSTADGFEHNGVNLGHFLTHLLEKESAPSRIVNSSLAH 180

Db 121 LHWINNAGVMMCPYSTADGFEHNGVNLGHFLTHLLEKESAPSRIVNSSLAH 180

Qy 181 HLGRHFHNLQGEKFNAGLAVCHSKLANILFTQELARRLKSGSVTTYSVHPGTVOSELV 240

Db 181 HLGRHFHNLQGEKFNAGLAVCHSKLANILFTQELARRLKSGSVTTYSVHPGTVOSELV 240

Qy 241 RHSSFMEMMMWLFSFFIKTPQOGAQTSLHCAITGELTISGNHPSDCHVAVMSAQARNET 300

Db 241 RHSSFMEMMMWLFSFFIKTPQOGAQTSLHCAITGELTISGNHPSDCHVAVMSAQARNET 300

Qy 301 IARRLMDV 308

Db 301 IARRLMDV 308

RESULT 9

US-10-205-823-227

Sequence 227, Application US/10205823

Publication No. US20030108963A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John E.

APPLICANT: Endege, Wilson O.

APPLICANT: Gannavarapu, Manjula

APPLICANT: Gorbacheva, Bella

APPLICANT: Hoersch, Sebastian

APPLICANT: Kamatekar, Shubhangi

APPLICANT: Monsey, Angela M.

APPLICANT: Glatc, Karen

APPLICANT: Zhao, Xumei

APPLICANT: Anderson, Dustin

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

FILE REFERENCE: MRI-044

CURRENT APPLICATION NUMBER: US/10/205,823

CURRENT FILING DATE: 2002-07-25

PRIOR APPLICATION NUMBER: 60/307,982

PRIOR FILING DATE: 2001-07-25

PRIOR APPLICATION NUMBER: 60/314,356

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/325,020

PRIOR FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 60/341,746

PRIOR FILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: 60/362,158

PRIOR FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 455

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 227

LENGTH: 318

TYPE: PRT

ORGANISM: Homo sapiens

US-10-205-823-227

Query Match 95.1%; Score 1577; DB 14; Length 318;

Best Local Similarity 98.7%; Pred. No. 1.2e-143;

Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MVELMPFLLLLPFLLYMAAPDIRKMLSSGVCSTSVQIPGKVVVVTGANTGIGKETAKE 60

Db 1 MVELMPFLLLLPFLLYMAAPDIRKMLSSGVCSTSVQIPGKVVVVTGANTGIGKETAKE 60

Qy 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAKGFLAEK 120

Db 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAKGFLAEK 120

Qy 121 LHWINNAGVMMCPYSTADGFEHNGVNLGHFLTHLLEKESAPSRIVNSSLAH 180

Db 121 LHWINNAGVMMCPYSTADGFEHNGVNLGHFLTHLLEKESAPSRIVNSSLAH 180

Qy 181 HLGRHFHNLQGEKFNAGLAVCHSKLANILFTQELARRLKSGSVTTYSVHPGTVOSELV 240

Db 181 HLGRHFHNLQGEKFNAGLAVCHSKLANILFTQELARRLKSGSVTTYSVHPGTVOSELV 240

Qy 241 RHSSFMEMMMWLFSFFIKTPQOGAQTSLHCAITGELTISGNHPSDCHVAVMSAQARNET 300

Db 241 RHSSFMEMMMWLFSFFIKTPQOGAQTSLHCAITGELTISGNHPSDCHVAVMSAQARNET 300

Qy 301 IARRLMDV 308

Db 301 IARRLMDV 308

RESULT 10

US-10-144-678A-339

Sequence 339, Application US/10144678A

Publication No. US20030157089A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Ranger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A. W.

APPLICANT: Hepler, William T.

APPLICANT: Hurst, John

APPLICANT: McNeill, Patricia D.

APPLICANT: Houghton, Raymond L.

APPLICANT: Vinals y de Baasols, Carlot

APPLICANT: Foy, Teresa M.

APPLICANT: Matanabe, Yoshihiro

APPLICANT: Deng, Ta

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427028

CURRENT APPLICATION NUMBER: US/10/144,678A

CURRENT FILING DATE: 2002-08-12

NUMBER OF SEQ ID NOS: 1033

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 339

LENGTH: 318

TYPE: PRT

ORGANISM: Homo sapiens

US-10-144-678A-339

Query Match 95.1%; Score 1577; DB 14; Length 318;

Best Local Similarity 98.7%; Pred. No. 1.2e-143;

Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MVELMPFLLLLPFLLYMAAPDIRKMLSSGVCSTSVQIPGKVVVVTGANTGIGKETAKE 60

Db 1 MVELMPFLLLLPFLLYMAAPDIRKMLSSGVCSTSVQIPGKVVVVTGANTGIGKETAKE 60

Qy 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAKGFLAEK 120

Db 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAKGFLAEK 120

QY 121 LHWINNAGVMMCPYSKTADGFEMHIGVNHGHLFTLLLEKLESAPSRIYVSSLAH 180
DB 121 LHWINNAGVMMCPYSKTADGFEMHIGVNHGHLFTLLLEKLESAPSRIYVSSLAH 180
QY 181 HLGRIHFHNLOGEKFYNAGLAAYCHSKLANILFTQELARLKSGSVTTYSVHPGTVOSELY 240
DB 181 HLGRIHFHNLOGEKFYNAGLAAYCHSKLANILFTQELARLKSGSVTTYSVHPGTVOSELY 240
QY 241 RHSSFRMMWMLFSPFIKTPOGAQOTRLHCALTEGLEILSGNHFSDCHVAMVSAQARNET 300
DB 241 RHSSFRMMWMLFSPFIKTPOGAQOTRLHCALTEGLEILSGNHFSDCHVAMVSAQARNET 300
QY 301 IARRLWDV 308
DB 301 IARRLWDV 308

RESULT 11
US-10-294-025-339
Sequence 339, Application US/10294025
Publication No. US20030185830A1
GENERAL INFORMATION:
APPLICANT: Stolx, John A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 2.0121.427C29
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-10-294-025-339

Query Match 95.1%; Score 1577; DB 14; Length 318;
Best Local Similarity 98.7%; Pred. No. 1,2e-143;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MVELMPELLLLLPFLYMAAPQIRKMLSSGVCTSTVQJPGKVVVVTGANTGIGETAYE 60
DB 1 MVELMPELLLLLPFLYMAAPQIRKMLSSGVCTSTVQJPGKVVVVTGANTGIGETAYE 60
QY 61 LAQRGARVYLACDVEKGEIVAKEIOTTGNOQVLRKLDSDTYSIRAWAGFAAEKH 120
DB 61 LAQRGARVYLACDVEKGEIVAKEIOTTGNOQVLRKLDSDTYSIRAFAGFLAEKH 120
QY 121 LHWINNAGVMMCPYSKTADGFEMHIGVNHGHLFTLLLEKLESAPSRIYVSSLAH 180
DB 121 LHWINNAGVMMCPYSKTADGFEMHIGVNHGHLFTLLLEKLESAPSRIYVSSLAH 180
QY 181 HLGRIHFHNLOGEKFYNAGLAAYCHSKLANILFTQELARLKSGSVTTYSVHPGTVOSELY 240
DB 181 HLGRIHFHNLOGEKFYNAGLAAYCHSKLANILFTQELARLKSGSVTTYSVHPGTVOSELY 240
QY 241 RHSSFRMMWMLFSPFIKTPOGAQOTRLHCALTEGLEILSGNHFSDCHVAMVSAQARNET 300
DB 241 RHSSFRMMWMLFSPFIKTPOGAQOTRLHCALTEGLEILSGNHFSDCHVAMVSAQARNET 300
QY 301 IARRLWDV 308
DB 301 IARRLWDV 308

RESULT 12
US-10-080-334-98
Sequence 98, Application US/10080334
Publication No. US20040002584A1
GENERAL INFORMATION:

APPLICANT: Pena, Carol E. A.
APPLICANT: Shimkets, Richard A
APPLICANT: Li, Li
APPLICANT: Shenoy, Suresh G
APPLICANT: Kekuda, Ramesh
APPLICANT: Splet, Kimberly A
APPLICANT: Vernet, Corine A. M.
APPLICANT: Malyskar, Uriel M
APPLICANT: Guo, Xiaojia
APPLICANT: Gusev, Vladimir Y
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc J
APPLICANT: Furtak, Katarzyna
APPLICANT: Tchernev, Velizar T
APPLICANT: Patturajan, Meera
APPLICANT: Gangolli, Esba A
APPLICANT: Padigaru, Muralidhara
APPLICANT: Liu, Xiaohong
APPLICANT: Baumgartner, Jason C.
APPLICANT: Gerlach, Valerie
APPLICANT: Spaderna, Steven K
APPLICANT: Zernusen, Bryan D
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE REFERENCE: 21402-275
CURRENT APPLICATION NUMBER: US/10/080,334
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/270,523
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/332,712
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/311,980
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/330,307
PRIOR FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: 60/278,796
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/281,521
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/276,677
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/311,595
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/270,220
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/274,295
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/318,526
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/286,548
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/291,765
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/270,797
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/276,400
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/270,810
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 98
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-10-080-334-98

Query Match 95.1%; Score 1577; DB 15; Length 318;
Best Local Similarity 98.7%; Pred. No. 1,2e-143;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MVELMPELLLLLPFLYMAAPQIRKMLSSGVCTSTVQJPGKVVVVTGANTGIGETAYE 60

Db 1 MVELMFPLLLLLPPLLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGETAKE 60
 QY 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAMAKGFABEKH 120
 Db 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAFKGFABEKH 120
 QY 121 LHWYINNAGVMCPYSKTADGFEHMGVNLGHFLTHLLEKLESAPSRIVNVSILAH 180
 Db 121 LHWYINNAGVMCPYSKTADGFEHMGVNLGHFLTHLLEKLESAPSRIVNVSILAH 180
 QY 181 HIGRIHFHNLQGEKFFYNAGLAYCHSKLANILFTQELARLKSGSVTTYSVHPGTVOSELY 240
 Db 181 HIGRIHFHNLQGEKFFYNAGLAYCHSKLANILFTQELARLKSGSVTTYSVHPGTVOSELY 240
 QY 241 RHSSFMKMMWMLFSFFIKTPQOGAOTRLHCAITGELILSGNHFSDCHVAVWSAQARNET 300
 Db 241 RHSSFMKMMWMLFSFFIKTPQOGAOTSLHCAITGELILSGNHFSDCHVAVWSAQARNET 300
 QY 301 IARRLMDV 308
 Db 301 IARRLMDV 308

RESULT 13

US-10-408-765A-3006
 ; Sequence 3006, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glemm, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 ; FILE REFERENCE: 660088.465
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3006
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-3006

Query Match 95.1%; Score 1577; DB 16; Length 318;
 Best Local Similarity 98.7%; Pred. No. 1,2e-143;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MVELMFPLLLLLPPLLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGETAKE 60
 Db 1 MVELMFPLLLLLPPLLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGETAKE 60
 QY 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAMAKGFABEKH 120
 Db 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAFKGFABEKH 120
 QY 121 LHWYINNAGVMCPYSKTADGFEHMGVNLGHFLTHLLEKLESAPSRIVNVSILAH 180
 Db 121 LHWYINNAGVMCPYSKTADGFEHMGVNLGHFLTHLLEKLESAPSRIVNVSILAH 180
 QY 181 HIGRIHFHNLQGEKFFYNAGLAYCHSKLANILFTQELARLKSGSVTTYSVHPGTVOSELY 240
 Db 181 HIGRIHFHNLQGEKFFYNAGLAYCHSKLANILFTQELARLKSGSVTTYSVHPGTVOSELY 240
 QY 241 RHSSFMKMMWMLFSFFIKTPQOGAOTRLHCAITGELILSGNHFSDCHVAVWSAQARNET 300
 Db 241 RHSSFMKMMWMLFSFFIKTPQOGAOTSLHCAITGELILSGNHFSDCHVAVWSAQARNET 300
 QY 301 IARRLMDV 308
 Db 301 IARRLMDV 308

Db 301 IARRLMDV 308

RESULT 14

US-10-131-410-147
 ; Sequence 147, Application US/10131410
 ; Publication No. US20030235915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SPECHT, THOMAS
 ; APPLICANT: HINZMANN, BERND
 ; APPLICANT: SCHMITT, ARMIN
 ; APPLICANT: PILARSKY, CHRISTIAN
 ; APPLICANT: DAHL, EDGAR
 ; APPLICANT: ROSENTHAL, ANDRE
 ; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST
 ; TITLE OF INVENTION: TUMORS
 ; FILE REFERENCE: SCH-1763
 ; CURRENT APPLICATION NUMBER: US/10/131,410
 ; CURRENT FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: 09/646,673
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: PCT/DE99/00908
 ; NUMBER OF SEQ ID NOS: 202
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 147
 ; LENGTH: 333
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-131-410-147

Query Match 95.1%; Score 1577; DB 14; Length 333;
 Best Local Similarity 98.7%; Pred. No. 1.3e-143;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVELMFPLLLLLPPLLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGETAKE 60
 Db 16 MVELMFPLLLLLPPLLYMAAPQIRKMLSSGVCSTVQLPGKVVVVTGANTGIGETAKE 75
 QY 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAMAKGFABEKH 120
 Db 61 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAFKGFABEKH 135
 QY 76 LAORGARVYLACRDVEKGEIVAKEIOTTGNOQVLRKLDLSDTKSIRAFKGFABEKH 135
 Db 121 LHWYINNAGVMCPYSKTADGFEHMGVNLGHFLTHLLEKLESAPSRIVNVSILAH 180
 QY 121 LHWYINNAGVMCPYSKTADGFEHMGVNLGHFLTHLLEKLESAPSRIVNVSILAH 180
 Db 136 LHWYINNAGVMCPYSKTADGFEHMGVNLGHFLTHLLEKLESAPSRIVNVSILAH 195
 QY 181 HIGRIHFHNLQGEKFFYNAGLAYCHSKLANILFTQELARLKSGSVTTYSVHPGTVOSELY 240
 Db 181 HIGRIHFHNLQGEKFFYNAGLAYCHSKLANILFTQELARLKSGSVTTYSVHPGTVOSELY 240
 QY 196 HIGRIHFHNLQGEKFFYNAGLAYCHSKLANILFTQELARLKSGSVTTYSVHPGTVOSELY 255
 Db 241 RHSSFMKMMWMLFSFFIKTPQOGAOTRLHCAITGELILSGNHFSDCHVAVWSAQARNET 300
 QY 256 RHSSFMKMMWMLFSFFIKTPQOGAOTSLHCAITGELILSGNHFSDCHVAVWSAQARNET 315
 Db 301 IARRLMDV 308
 Db 316 IARRLMDV 323

RESULT 15

US-10-131-410-198
 ; Sequence 198, Application US/10131410
 ; Publication No. US20030235915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SPECHT, THOMAS
 ; APPLICANT: HINZMANN, BERND
 ; APPLICANT: SCHMITT, ARMIN
 ; APPLICANT: PILARSKY, CHRISTIAN
 ; APPLICANT: DAHL, EDGAR
 ; APPLICANT: ROSENTHAL, ANDRE
 ; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST

```

; TITLE OF INVENTION: TUMORS
; FILE REFERENCE: SCH-1763
; CURRENT APPLICATION NUMBER: US/10/131,410
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/646,673
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: PCT/DE99/00908
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 198
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-410-198

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Query Match          95.1%; Score 1577; DB 14; Length 335;
Best Local Similarity 98.7%; Pred. No. 1,3e-143;
Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

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QY 1 MVELMPELILLPLFLYMAAPQIRKMLSSGVCSTVQLPGKYVVVTGANTGIGKETAKE 60
   |||||
Db 18 MVELMPELILLPLFLYMAAPQIRKMLSSGVCSTVQLPGKYVVVTGANTGIGKETAKE 77
   |||||

QY 61 LAQGAAYVLACRDVEKGLVAKEIOTTGNQOVLRKLDLSDTKSIRAMAKGFKAEKH 120
   |||||
Db 78 LAQGAAYVLACRDVEKGLVAKEIOTTGNQOVLRKLDLSDTKSIRAFKGTAEKH 137
   |||||

QY 121 LHWINNAGVWMCPSKTDGFMHIGVNLGHFLTLHLLEKLEKESAPSRIYVSSLAH 180
   |||||
Db 138 LHWLNNAGVWMCPSKTDGFMHIGVNLGHFLTLHLLEKLEKESAPSRIYVSSLAH 197
   |||||

QY 181 HLGRIHFHNLOGEKFYVAGLAYCHSKLANILFTQELARRLKSGVTTYSVHPGTVOSELY 240
   |||||
Db 198 HLGRIHFHNLOGEKFYVAGLAYCHSKLANILFTQELARRLKSGVTTYSVHPGTVOSELY 257
   |||||

QY 241 RHSSFMKMMWMLFSFPIKTPQGAQTRLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 300
   |||||
Db 258 RHSSFMKMMWMLFSFPIKTPQGAQTSLHCALTEGLEILSGNHFSDCHVAVWSAQARNET 317
   |||||

QY 301 IARRIMDV 308
   |||||
Db 318 IARRIMDV 325
   |||||

```

Search completed: October 13, 2004, 18:24:53
 Job time : 133 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 18:05:04 ; Search time 40 Seconds

(without alignments)
760.112 Million cell updates/sec

Title: US-10-021-002-2

Perfect score: 1659
Sequence: 1 MWELMPFLLLLPFLLYMA.....RNERTARLMDVIVTCMASQ 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR 79: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	29.3	350	2 T48275	hypothetical prote
2	476	28.7	304	2 T44727	probable oxidoredu
3	475.5	28.7	321	2 T02520	probable oxidoredu
4	470	28.3	303	2 E70848	probable oxidoredu
5	466.5	28.1	320	2 S42651	hypothetical prote
6	464.5	28.0	311	2 H70829	hypothetical prote
7	462.5	27.9	317	2 T10561	hypothetical prote
8	446	26.9	311	2 AD2021	hypothetical prote
9	440	26.5	316	2 D84206	probable oxidoredu
10	438	26.4	309	2 C83017	probable short cha
11	430.5	25.9	323	2 E87298	hypothetical prote
12	423.5	25.5	317	2 C70863	hypothetical prote
13	419.5	25.3	332	2 T13447	hypothetical prote
14	419.5	25.3	336	2 H75255	oxidoreductase, sh
15	406.5	24.5	339	2 T41570	hypothetical prote
16	400.5	24.1	333	2 T19314	hypothetical prote
17	389.5	23.5	400	2 C75365	dehydrogenase, sh
18	386.5	23.3	301	2 AE3155	dehydrogenase Atus
19	376.5	22.7	322	2 T04022	hypothetical prote
20	373.5	22.5	398	2 T33973	hypothetical prote
21	370.5	22.3	379	2 T23592	hypothetical prote
22	363	21.9	294	2 T05381	hypothetical prote
23	360.5	21.7	339	2 B86906	oxidoreductase yxd
24	349.5	21.1	329	2 T15910	hypothetical prote
25	349	21.0	204	2 T46363	hypothetical prote
26	342.5	20.6	925	2 T16235	hypothetical prote
27	341	20.6	311	2 T37155	probable oxidoredu
28	336	20.3	298	2 A47089	probable oxidoredu
29	323.5	19.5	297	2 S19842	probable oxidoredu

30	323.5	19.5	323	2 T29260	hypothetical prote
31	322	19.4	400	2 S20941	protochlorophyllid
32	321	19.3	397	2 S71468	protochlorophyllid
33	318.5	19.2	329	2 A12023	protochlorophyllid
34	314	18.9	315	2 T23597	hypothetical prote
35	314	18.9	398	2 JC4146	protochlorophyllid
36	308	18.6	312	2 T17150	probable oxidoredu
37	307	18.5	388	2 S59354	protochlorophyllid
38	306	18.4	400	2 S50167	protochlorophyllid
39	305	18.4	388	2 S04783	protochlorophyllid
40	299	18.0	296	2 D82515	ketoreductase XF27
41	299	18.0	401	2 T00897	protochlorophyllid
42	297.5	17.9	313	2 S08406	protochlorophyllid
43	297	17.9	401	2 T08926	protochlorophyllid
44	295.5	17.8	346	2 T51377	hypothetical prote
45	285.5	17.2	322	2 S76636	hypothetical prote

ALIGNMENTS

RESULT 1
T48275
hypothetical protein T22P11.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48275
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, A.; Cross-References: UNIPROT:Q9L248; EMBL:AL162971
A:Reference number: 224490
A:Accession: T48275
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <BEV>
A:Cross-References: UNIPROT:Q9L248; EMBL:AL162971
A:Experimental source: cultivar Columbia; BAC clone T22P11
C:Genetics:
A:Map position: 5
A:Introns: 40/1; 136/2; 163/1; 214/2; 240/3; 269/1; 284/3
A>Note: T22P11.130
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match	Score	DB 2	Length	350;
Best Local Similarity	37.1%	Pred. No. 5,8e-32;		
Matches	114;	Conservative	55;	Mismatches 108; Indels 30; Gaps 5;
QY	34	TSVQLPGKVVVVTGANTGIGETAKELAQGAPVYLACROVEKELVAKELQTTGNOQ	93	
DB	26	TGGIDATNLTALITGGTGGIGETARVLSKGAHVIGARNNGAENAKTEILRONANAR	85	
QY	94	VIVRKLDSDTKSIRAMAKGFVAKSKHLHWI-----NNAGVMCP	134	
DB	86	VTLQDLDSISIKAFREFHALLPLNLTMTSLGIFKAPAPFLNAGVMCP	145	
QY	135	YKTIADGFPMHIGVNLGHFLLTHLLLEKLSASAS-----RIVVSSLAH---HLGITH	186	
DB	146	YOLSEDEGLHGFATNHHGFLLTNLLDMKNTATSGEGRILNWSVAHLYYQESIQ	205	
QY	187	FNLQEKFNYNAGLVCHSKLANILFTOELARLKGSGV---TTSVSHGTVQSEILVRSS	244	
DB	206	FESINDICYSKRAVQSGSKLANIILHANELSQLODEGVNITANSVHGLITNLFQHTA	265	
QY	245	PRKMMWMLSEFPI-KTPOGAGTRHLCALTEGLEILSGNHPSDCHVAVASQARNETAR	303	
DB	266	LIMRFKFPSPFLMKNIPOGAATTCVVALHPSVKGVTKGFADCNVEVPSKLARDETLAQ	325	
QY	304	RLMDVIV 310		
DB	326	KLMDSV 332		
RESULT 2	T44727			

Probable oxidoreductase [imported] - Mycobacterium leprae
 C/Species: Mycobacterium leprae
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T44727
 R/James, K.D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1998
 A/Reference number: Z22831
 A/Accession: T44727
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-304 <QMA>
 A/Cross-references: UNIPROT:Q9ZBM5; EMBL:AL035159; PIDD:CAA22691.1
 A/Experimental source: cosmid B1450
 C/Genetics:
 A/Note: MLCB1450.07
 C/Superfamily: ribitol dehydrogenase, short-chain alcohol dehydrogenase homology

Query Match 28.7%; Score 476; DB 2; Length 304;
 Best Local Similarity 41.0%; Pred. No. 3.2e-11;
 Matches 120; Conservative 47; Mismatches 102; Indels 24; Gaps 9;

QY 35 STVQLP---GKVVYVGTANTGIGETAKELAORGARVYLACRDVKEGELVAKEIQTTCN 91
 Db 5 TTADIPQGTGRVAVITGANTGLGYQALALAEHGAHVLAVERLKGDAARITATSQ 64
 QY 92 QQVILVKLDSPTKSIKAWKGFKAEEKLHWINNAGVMMCPYSKTADGFEMHIGVNL 151
 Db 65 NVVALGELDLASLESRAAKKQKRSYDHDLDLNNAGVMTPKSTTKGFELOGTNHL 124
 QY 152 GHFLTHLLLEKIKESAPRIVNSSLAHL-GRIFHNLQGEKFNAGLAYCHSKLANI 210
 Db 125 GHFAFGTGLDRLPLTVGSRVITVSSLSHRLFDIHFNDLOWECNNRVAAGOSKLANL 184
 QY 211 LFFQELARLRKSGSVTVSY--HPTVQSELVHSSFFMMWMLFS---FPIKTPQGA 264
 Db 185 LFVTEQLQRRL-ARQTTIAVAHAPGSRRLTR--TLPLAIPESVALFLTDAAATCA 241
 QY 265 QTRHLCALTEGLEILSGNHFSD-----CHVAWSAQRNETIAR--RLMDV 308
 Db 242 LPTLRATADAA--VLGGYFPGDGFALRIGHPRVAVNSGKSHDVROQLTMVAV 292

RESULT 3
 T02520
 probable oxidoreductase [imported] - Arabidopsis thaliana
 N/Alternate names: hypothetical protein F13M22.4
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
 C/Accession: T02520; A84794
 R/Rounseley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998
 A/Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.
 A/Reference number: Z14677
 A/Accession: T02520
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-321 <ROU>
 A/Cross-references: UNIPROT:O80924; EMBL:AC004684; NID:G3236234; PID:G3236237
 A/Experimental source: cultivar Columbia
 R/Lin, X.; Kaul, S.; Rounseley, S.D.; Shao, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: A84420; XUID:20083487; PMID:10617197
 A/Accession: A84794
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-321 <STO>
 A/Cross-references: GB:AB002093; NID:G3236237; PIDD:AA03625.1; GSPDB:GM00139
 C/Genetics:
 A/Gene: Atg37540; F13M22.4
 A/Map position: 2

A/Introns: 40/1; 117/2; 144/1; 195/2; 221/3; 250/1; 265/3
 C/Superfamily: ribitol dehydrogenase, short-chain alcohol dehydrogenase homology

Query Match 28.7%; Score 475.5; DB 2; Length 321;
 Best Local Similarity 38.9%; Pred. No. 3.7e-11;
 Matches 112; Conservative 48; Mismatches 117; Indels 11; Gaps 4;

QY 34 TSTVQLPGRVYVGTANTGIGETAKELAORGARVYLACRDVKEGELVAKEIQTTCNQ 93
 Db 26 TQADASHLTAITIGTSGIGLEAARVLAARGAVITIAANPRANESKEMILQNNPNAR 85
 QY 94 VLVRKLDSPKSIKAWKGFKAEEKLHWINNAGVMMCPYSKTADGFEMHIGVNLGH 153
 Db 86 VDIQIDVSSIKSRSDVDQFLNVLNPLNINAGVMFPKPLTLDGIESGPAATHIGH 145
 QY 154 FLTHLLLEKIKESA----PSRIVNSSLAH--HLGRIFHNLQGEKFNAGLAYCHS 205
 Db 146 FLTNLLDLKMKRSRARSVGQGRIVNLSIAHTYVSEGIKFGINDPAGSERRAYGGS 205
 QY 206 KLANILFTQELARLRKSGV--TTSVHPQTQSELVHSSFFMMWMLFSF-FIKTPQG 262
 Db 206 KLSNLSNLSNLSRRLQEGVNTITNSVHPQLVTTNLFRYSGFEMKVPFRANTFLFWKXIPQ 265
 QY 263 GAQTRHLCALTEGLEILSGNHFSDCHVAWSAQRNETIARRLMDVIV 310
 Db 266 GAATTCYVALHPDLEGVTKGKFGDCNIVAPSKPATNNSLADKLMDPSV 313

RESULT 4
 E70848
 Probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)
 C/Species: Mycobacterium tuberculosis
 C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C/Accession: E70848
 R/Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felkwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G. A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A/Reference number: A70500; MUID:98255987; PMID:9634230
 A/Accession: E70848
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-303 <COL>
 A/Cross-references: UNIPROT:O53613; GB:AL021428; GB:AL123456; NID:G3261514; PIDD:CAA1624
 A/Experimental source: strain H37RV
 C/Genetics:
 A/Gene: Rv0068
 C/Superfamily: ribitol dehydrogenase, short-chain alcohol dehydrogenase homology
 F/15-208/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 28.3%; Score 470; DB 2; Length 303;
 Best Local Similarity 40.6%; Pred. No. 9.7e-11;
 Matches 113; Conservative 46; Mismatches 109; Indels 10; Gaps 5;

QY 41 GKVVYVGTANTGIGETAKELAORGARVYLACRDVKEGELVAKEIQTTCNQVLRKLD 100
 Db 14 GRFAVITGANTGIGEFPAALAAHGAHVLAVERLKGDAARITEA-PGAEEVELEND 73
 QY 101 LSPDKSIKAWKGFKAEEKLHWINNAGVMMCPYSKTADGFEMHIGVNLGHFLTHLL 160
 Db 74 LTIASLRARAAQAQKSHQIDILINNAGVMYPRQTTDADGEMQGTNHLGHFALTGL 133
 QY 161 LEKIKESAPRIVNSSLAHL-GRIFHNLQGEKFNAGLAYCHSKLANILFTQELAR 219
 Db 134 IDRLPLVAGSRVYVITISVGRIRAPALHFPDLQWERRYRVAAYGQAKLANLFLTEQLQR 193
 QY 220 LKSGGVY-TTSVHPQTQSELVHSSFFMMWMLFSF-FIKTPQGAQRLCA---LRE 274
 Db 194 LAPGGTIIAASHPGVSNTEVAVNMPRLVAVAAIAPLMQDAEELGALPTLRATDPAYR 253
 QY 275 GLEILSGNHFSDCH---VAWSAQRNETIARRLMDV 308

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AD2021
R/Kaneko, T.; Nakamura, Y.; Wolz, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yaeuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AD2021
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-311 <STO>
A/Cross-references: UNIPROT:Q8W93; GB:BA000019; PIDN:BAE73421.1; PID:G17130812; GSPDB:G
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: alr1722
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 26.8%; Score 446; DB 2; Length 311;
Best Local Similarity 38.8%; Pred. No. 9e-29;
Matches 108; Conservative 54; Mismatches 104; Indels 12; Gaps 5;

QY 41 GKVVVVGANTGIGKETAKELAQGARVYLACRDEKSELVAKETITGNOQVLRKD 100
DB 16 GRLLVVGSSSGGYETARVANKQASVITAVNLRKNGKALAKIQQNKDADVKLELD 75
QY 101 LSDTKIRAWAKGFKAEKELHVINNAGVMCPYSKTDGPEMHIGVNLGHFLTHLL 160
DB 76 LANLAVKKNFENPRKRYLRDLIDINNAGVMEPYKTDGPELGTGTHLGHFLTQGL 135
QY 161 LKIKESAPRIVVSSLAHHLGRIFHNIOGE-KRYNAGLAYCHSKLANILFTQELAR 219
DB 136 LEFLISTEGSRIVVSSGANNMKIDFDDLNMEQRVYAKWKAQDSKLANILFTYELDKR 195
QY 220 LKSGGVTTY--SVHPGVQSELVHSSFMKMMWLFSFKTPQOAGCTRLCALTEGP- 276
DB 196 LKXNGIDITLVASHPGWTATLORTAGI--VXVINGVIAQDITWALTLAAALEAGLX 253
QY 277 -EILSGNHSDOCHVAVSAQ---ANETIARLMDV 308
DB 254 GAIEYFGNGFMENRGYPIKESNELSKDQALAKKLMV 291

RESULT 9
DB4206
probable oxidoreductase [imported] - Halobacterium sp. NRC-1
C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: DB4206
R/Ni, M.V.; Kennedy, S.P.; Mahafas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A/Title: Genome sequence of Halobacterium species NRC-1.
A/Reference number: AB4160; MUID:20504483; PMID:11016950
A/Accession: DB4206
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-316 <STO>
A/Cross-references: UNIPROT:Q9HR22; GB:AE004437; NID:G10580084; PIDN:AA619016.1; GSPDB:G
C/Genetics:
A/Gene: ya101
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 26.5%; Score 440; DB 2; Length 316;
Best Local Similarity 39.3%; Pred. No. 2.8e-28;
Matches 119; Conservative 41; Mismatches 119; Indels 24; Gaps 7;

QY 28 LSSGVCSTVLP---GKVVVVGANTGIGKETAKELAQGARVYLACRDEKSELVAK 84
DB 1 MSSDDMTAALPDQGRVVTGANSGLGFETRAFAAGAHVWACSTRGEDARD 60
QY 85 IOTTGNOQVLRKDLSDTKIRAWAKGFKAEKELHVINNAGVMCPYSKTDGPEM 144

DB 61 TVAEPLGASLTVHEDLDLALDVAAPFADWTAEKDSLHVLANNAGVMAIRSETRADQET 120
QY 145 HIGVNLGHFLTHLLLEKKE-SAPSRIVVSSLAHHLGRIFHNIOGEKFNAGLAYC 203
DB 121 QGVVNLGHVNLITGLLGVLRITGSETRVVTQSSGARREIRIDFEDLOHAEVQKWEAYS 180
QY 204 HSKLANILFTQELARRK--GSGVTTYVHPGVQSELVH-----SSEFRMMWLFSF 256
DB 181 OSKLANILFAYELDRRLRAASASVTSVACHPGVATVLRQGPQACSRILAMRAANA 240
QY 257 I--XTPOGAGTRLHCAITGCELLSGNHSDOCHVAVV-----SAQARNETIARL 305
DB 241 LVQSAEGGAMPILYATNPSID--GGEYIGPGVLMRHPERQPSARSREDTARRL 298
QY 306 MDV 308
DB 299 WTV 301

RESULT 10
C83017
probable short chain dehydrogenase PA5031 [imported] - Pseudomonas aeruginosa (strain PA
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: C83017
R/Stover, C.K.; Pham, X.Q.; Eryin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardi, K.; Lim,
N.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: AB2950; MUID:20437337; PMID:10984043
A/Accession: C83017
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-309 <STO>
A/Cross-references: UNIPROT:Q9HUB6; GB:AE004916; GB:AE004091; NID:G9551315; PIDN:AA60841
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA5031
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 26.4%; Score 438; DB 2; Length 309;
Best Local Similarity 38.8%; Pred. No. 4e-28;
Matches 111; Conservative 44; Mismatches 113; Indels 18; Gaps 6;

QY 38 QLPKVVVVGANTGIGKETAKELAQGARVYLACRDEKSELVAKETITGNOQVLR 97
DB 11 QVARRLALVIGANSGLQWQAARTLAGKATVWVACRRBQARARALDEYPOARLELA 70
QY 98 KLDLSDTKIRAWAKGFKAEKELHVINNAGVMCPYSKTDGPEMHIGVNLGHFLT 157
DB 71 DLDLADLASIRPACAGRQHRARLDLFNNAQWFLPLRTRDGFEMQGTNLGHFLT 130
QY 158 HLLKESAPRIVVSSLAHHLGRIFHNIOGEKFNAGLAYCHSKLANILFTQEL 217
DB 131 GLILDSILAAPRRVIVGWTSGFQFGLPLDDLNMEQRVYAKWKAQDSKLANILF 190
QY 218 RLKSGGVTTYV--HPGVQSEL-----VHSSFMKMMWLFSFKTPQOAGCTRL 268
DB 191 RRAQQRVVLQSLAHPGVAATNLOVAPAPMSSSRGRWAKVANGAFQSAEMGALPAL 250
QY 269 HCAITE---GLEILSGNHSDOCH---VAVSAQARNETIARLM 306
DB 251 -SALTQWRWYGAVGPDRLWETRGVPAARIRRNADGLAKRLM 295

RESULT 11
BB7298
hypothetical protein C03098 [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: BB7298

R;Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Lab, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolton B.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapir, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87298
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-323 <STO>
A:Cross-references: UNIPROT:Q9AB36; GB:AE005673; NID:G13421559; PIDN:AAK22385.1; GSPDB:G
C:Genetics:
A:Gene: C00398
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.9%; Score 430.5; DB 2; Length 323;
Best Local Similarity 38.6%; Pred. No. 1,7e-27;
Matches 117; Conservative 35; Mismatches 110; Indels 41; Gaps 9;

39 LPKVVVVVTGANTGIGKETAKELAQRGARYVLAQDVKEGELVAKETQTTGNOQVLRK 98
24 LSGVVAIVTGAITGIVETALALAGAEVITARRKPELGEVANAINEBAGSKRVSPGM 83
99 LIDSDTISR---AMAKGFAEKHLVWINNAGVMMCPYSTADGFEMHIGVNLGHF 154
84 LIDSLERAIHFVAVWG-----DRIDILINNAVAPLMRTADGFEMQFGTNLGHF 137
155 LITLHLEKLKES-----PSRIYVSSLAHLGRIFHNLO-GEKYNAGLAAYCSKLA 208
138 LLSVLALPNLJAGKASGKRSRLVSLSSIGHRSRGIHFDPNPTTREPKEKAYGQAKTA 197
209 NIEFQELARLKSGVTYSVHPTQSEIVRHSF--WRMMWML-----PSFET 257
198 NSLFVNGEDRFKQGVHANAAMVCGILTPQLRHLPEBGRALGMDENDQPREGF----- 253
258 KTPQOQAQTRHLCALTEGLEILSGNHFSDCHA-----W-VSAQARNETIARLMD 307
254 KTEQGAATSVMAVAGSELEGVGLYLEDGQALPMGSKENPMTGVMHAPALDRLMD 313
308 VIV 310
314 LSV 316

RESULT 12
C70863
hypothetical protein Rv2263 - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: C70863
R;Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajadaram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634220
A:Accession: C70863
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-317 <COL>
A:Cross-references: UNIPROT:O53537; GB:AL021925; GB:AL123456; NID:G2909556; PIDN:CAA1730
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: Rv2263
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F:15-209/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 25.5%; Score 423.5; DB 2; Length 317;
Best Local Similarity 35.4%; Pred. No. 6.3e-27;
Matches 109; Conservative 59; Mismatches 109; Indels 31; Gaps 9;
28 LSSGCVSTVQLPKVVVVVTGANTGIGKETAKELAQRGARYVLAQDVKEGELVAKETQTT 87

1 MAKDVAIVPDISGLAITTANSGLFGCLRRISAAADIVYAIRNAKEAAVEERT 60
88 ITGNOQVLRKLDSDTTSIRAMAKGFAEKHLVWINNAGVMMCPYS-XTADGFEMH 146
61 AVPDAKLITKMLDSSLSVAALGQMAADRPIDLLINNAGVMTTPERRVTTAOGFELQF 120
147 GVNHLGHFLTHLLEKLKESAPSAIYVSSLAHLGRIFHNLO-GEKYNAGLAAYCSK 206
121 GSNHLGHFLTAHLFLPFAAQRAVSLSSLAARRGIHFDDIQFERSVAPMTAYGSK 180
207 LANILFTQELARLK--GSGVTYSVHPTQSEIVRHSF--WRMMWML-----PSFET 253
181 LAVMFARLEDRRSAAAGWGIISNAHGLTKTNLIQIAGPHGRDKPALMERLYTSRIF 240
254 SFET-KTPQOQAQTRHLCALT--EG-----LEILSGNHFSDCHAAMVSAQARNET 300
241 APFLMQEIEEGILPALYAAATPQADGAFYGPGRGYEAVAGG---VREAKVPAARND 296
301 IARRLMDV 308
297 DSKRLMEV 304

RESULT 13
T13447
hypothetical protein T19F6.40 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13447
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bandrolf, I.; Mei submitted to the Protein Sequence Database, July 1999
A:Reference number: Z17587
A:Accession: T13447
A:Molecule type: DNA
A:Residues: 1-332 <BEV>
A:Cross-references: UNIPROT:O22985; EMBL:AL109619; GSPDB:GN00062; ATSP:T19F6.40
A:Experimental source: cultivar Columbia; BAC clone T19F6
C:Genetics:
A:Gene: ATSP:T19F6.40
A:Map position: 4
A:Intons: 41/1, 118/2, 145/1, 197/2, 224/3, 254/1, 269/3
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.3%; Score 419.5; DB 2; Length 332;
Best Local Similarity 36.5%; Pred. No. 1.4e-26;
Matches 109; Conservative 53; Mismatches 112; Indels 25; Gaps 6;

34 TSTVOLPKVVVVVTGANTGIGKETAKELAQRGARYVLAQDVKEGELVAKETQTTGNOQ 93
27 TENCDSLRSITAVITATGIGETARVLAQKARLIFPARVKAEBEAKERIVSEFPETE 86
94 VIVRLDSDTTSIRAMAKGFAEKHLVWINNAGVMMCPYSTADGFEMHIGVNLGH 153
87 IVVMKLDSLSASVAFADPESLDLPMLLINNAKLAHHAISDEIDMTFATNYIGH 146
154 FLTHLLEKLKES-----PSRIYVSS-----LAHLGRIFHNLO-GEKYNAG 199
147 FLTHLLEKLKES-----PSRIYVSS-----LAHLGRIFHNLO-GEKYNAG 199
200 LAYCSKLANILFTQELARLK--GSGVTYSVHPTQSEIVRHSF--WRMMWML-----PSFET 253
203 RYVALSKLANVHTLESRLQKIGANVTAVNCVHGAVRTPLTRDRBSLLTDVLFLLASK 262
256 FIKTPQOQAQTRHLCALTEGLEILSGNHFSDCHAAMVSAQARNETIARLMD---DVIVT 311
263 LKTVPQAATTCVYATNPRLVNVGKVFETDCCNETTPTGCLGNSSEATKLAASHILVT 321

RESULT 14
H75255
oxidoreductase, short-chain dehydrogenase/reductase family - *Deinococcus radiodurans* (s
C:Species: *Deinococcus radiodurans*

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: H75255
 R/Witte, O.; Eissen, J.A.; Heitelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.D.;
 M.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MIMD:20036896; PMID:10567266
 A/Accession: H75255
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-1336 <WHI>
 A/Cross-references: UNIPROT:Q9R899; GB:AE002089; GB:AE000513; NID:g6460427; PIDD:AAFI213
 A/Experimental source: strain R1
 C/Genetics:
 A/Map position: 1
 C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 25.3%; Score 419.5; DB 2; Length 336;
 Best Local Similarity 38.6%; Pred. No. 1,4e-26;
 Matches 112; Conservative 32; Mismatches 125; Indels 21; Gaps 6;

QY 37 VQLPGKVVVTGANTGIGKETAKELAQGARYVLAQDVEKGLYAKETITGNQOVLV 96
 DB 39 VDLKGTAVVTGASGIGTETARALLAGAHVILPVDRAKGERVAELRQSTGTVELY 98
 QY 97 RKLDLSDTYSIRAMAKGFABEKGHLHWINNAGVMKCPYSKTADGFEMHIGVNLGHFL 156
 DB 99 -DIDLGSLSAVRRGAIEIRIQLAPRIHILINNAGVATPQSRVTDGFEITFGTNHGHFL 157
 QY 157 THLLKLEKASAPSRIVNSSLAHNGRIHFNLQGEKF--YNAGLA YCHSKLANILFTQE 215
 DB 158 TRSLPALMAAARVVALTSGRSRSDIYMDLNFERRPYDPMAYGQSKTANALFVAG 217
 QY 216 IAAELKSGVTTYVHPGVQSELYVHSSF--MAMWMA-----LFSFPIKTPQQAQTRL 268
 DB 218 LFORVADQGLTANAVHPGIMTGLQKFEVPLEDQRMQDEHGTLPVFKTPAEGASTSV 277
 QY 269 HCAITGELTSGNHFSDC-HVAMVSAQAARNETI-----ARRLM 306
 DB 278 WAATSPQLGVGGLPLEDLOHSTPLEDSAPNPLFGYKPYALDHESARRLM 327

RESULT 15

T41570
 hypothetical protein SPC736.13 - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T41570
 R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
 submitted to the EMBL Data Library, May 1998
 A/Reference number: Z21991
 A/Accession: T41570
 A/Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1339 <WCO>
 A/Cross-references: UNIPROT:Q74959; EMBL:AL023705; PIDD:CAA19277.1; GSPDB:GN00068; SPDB:
 A/Experimental source: strain 972h-; cosmid C736
 C/Genetics:
 A/Map position: 3
 A/Map position: 3

Query Match 24.5%; Score 406.5; DB 2; Length 339;
 Best Local Similarity 35.7%; Pred. No. 1.6e-25;
 Matches 101; Conservative 60; Mismatches 107; Indels 15; Gaps 5;

QY 39 LRGKVVVVCANIGIKETAKELAQGARYVLAQDVEKGLYAKETITGNQOVLV 98
 DB 40 LTRKVALLVGSSGGIGVTALELARKAKYVLAQRNEEKYQKVMKQIHDEVHSHKIRFLR 99
 QY 99 LIDLSTKSIAMAKGFABEKGHLHWINNAGVMKCPYSKTADGFEMHIGVNLGHFL 158

DB 100 LIDLDFESVYQAABSFIAKEEKHLVNNAGINPPELTKGVEIQITNYSHYLFT 159
 QY 159 LLEKLEKESAPS-----RIVNSSLAH--HLGRIHFNLQGEKRYNAGLA-YCHSKLA 208
 DB 160 LLPTLRTABECRPGDVRIVHVASIAYLAQAPSGIYFPDLNPHYLIGTFARYGOSKYA 219
 QY 209 NILEFTGLARLKSGVTTYVHPGVQSELYVHSSFMMWMA-----LFSFPIKTPQQAQ 265
 DB 220 QILYSIALARLEKXYGIVSVLHPGVTRTELTRYSPTPAKLEKSVFOYLLDPIRGAM 279
 QY 266 TRLHCALTEGL--EILSGNHFSDCHVAMVSAQAARNETIARRLM 306
 DB 280 TSLVATSPKISKEHLNGAFTALAQGILHRAHDPAFVEELY 322

Search completed: October 13, 2004, 18:14:03
 Job time : 53 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2004, 18:04:53 ; Search time 74 Seconds
(without alignments)

2457.005 Million cell updates/sec

Title: US-10-021-002-2

Perfect score: 1659
Sequence: 1 MVELMPFLILLLPFLILYMA.....RNETIARRLMDVIVTCMAQ 316

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1577	95.1	318	1 RDHB_HUMAN	Q8C122 homo sapien
2	1577	95.1	318	2 CAG3461	Cag3461 homo sapi
3	1347.5	81.2	316	1 RDHB_MOUSE	Q9YF11 m retinol d
4	1291	77.8	300	2 Q9RLB8	Q9YF18 mus musculu
5	1279	77.1	293	2 Q9RLB8	Q9YF18 mus musculu
6	1259.5	75.9	407	2 Q9RLB8	Q9YF18 mus musculu
7	1259.5	75.9	407	2 Q9RLB8	Q9YF18 mus musculu
8	1129	68.1	316	1 RDHC_HUMAN	Aa991067
9	1126	67.9	316	1 RDHC_BOVIN	Q96N88 homo sapien
10	1068	64.4	316	1 RDHC_MOUSE	P59837 bos taurus
11	961	57.9	319	2 Q6D678	Q6D678 mus musculu
12	832	50.2	188	2 Q9RLB8	Q9YF18 mus musculu
13	799.5	48.2	291	2 Q6D678	Q6D678 mus musculu
14	762.5	46.0	331	2 Q6N749	Q6N749 brachydanto
15	762.5	46.0	331	2 AAH6739	AaH6739 brachydanto
16	747.5	45.1	336	2 Q7QJL8	Q7QJL8 anophelies g
17	733.5	44.2	330	2 Q9V4Q3	Q9V4Q3 drosophila
18	733	44.2	325	2 Q8M2G9	Q8M2G9 drosophila
19	731.5	44.1	330	2 Q9V4Q2	Q9V4Q2 drosophila
20	728	43.9	300	2 Q9V4Q2	Q9V4Q2 drosophila
21	724	43.6	331	2 Q9V4P9	Q9V4P9 drosophila
22	718	43.3	331	2 Q7Q686	Q7Q686 anophelies g
23	706.5	42.6	331	1 RDHD_HUMAN	Q8N177 homo sapien
24	705.5	42.5	331	1 Q6UX79	Q6UX79 homo sapien
25	705.5	42.5	331	2 AAQ88837	AaQ88837 homo sapi
26	707.5	42.3	334	1 RDHD_MOUSE	Q8C6E7 mus musculu
27	699.5	42.2	329	2 Q6GFF0	Q6GFF0 xenopus lae
28	695.5	41.9	318	2 Q6P001	Q6P001 brachydanto
29	695.5	41.9	318	2 AAH65890	AaH65890 brachydanto
30	689	41.5	296	2 Q6MKN1	Q6MKN1 drosophila
31	681	41.0	318	2 Q6D672	Q6D672 brachydanto

32	680.5	41.0	314	2 Q6P3N2	Q6P3N2 xenopus tro
33	680.5	41.0	314	2 AAH63926	AaH63926 xenopus t
34	680	41.0	296	2 Q7QJL8	Q7QJL8 anophelies g
35	672.5	40.5	406	2 Q9W404	Q9W404 drosophila
36	641.5	38.7	336	1 RDHE_HUMAN	Q9N185 homo sapien
37	638	38.5	334	1 RDHE_MOUSE	Q9N185 mus musculu
38	606.5	36.6	377	2 Q6UX79	Q6UX79 homo sapien
39	606.5	36.6	377	2 AAQ88829	AaQ88829 homo sapi
40	585	33.3	309	2 Q7Q348	Q7Q348 brachydanto
41	554.5	33.4	321	2 Q9L618	Q9L618 oryza sativ
42	543.5	32.8	327	2 Q6E6H7	Q6E6H7 homo sapien
43	539.5	32.5	260	2 Q6G6H8	Q6G6H8 homo sapien
44	535.5	32.3	288	2 Q7QJL8	Q7QJL8 anophelies g
45	525.5	31.7	336	2 Q9VE80	Q9VE80 drosophila

ALIGNMENTS

RESULT 1	ID	RDHB_HUMAN	STANDARD	PRT	318 AA.
AC	Q8C122	Q9NRWC	Q9Y391		
DT	10-OCT-2003	(Rel. 42, Created)			
DT	10-OCT-2003	(Rel. 42, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DE	Retinol dehydrogenase 11 (EC 1.1.1.1-)	(Retinal reductase 1) (RdR1)			
DE	(Prostate short-chain dehydrogenase/reductase 1) (HCV core-binding protein				
DE	short-chain dehydrogenase/reductase 1) (HCV core-binding protein				
DE	HCBP12) (CGI-82)				
GN	Name=RdH11, Synonyms=PSDR1, ARSDR1;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Prostate;				
RX	MEDLINE=21139101; PubMed=11245473;				
RA	Lin B., White J.T., Ferguson C., Wang S., Vessella R., Bumgarner R.,				
RA	True L.D., Hood L., Nelson P.S.,				
RT	"Prostate short-chain dehydrogenase reductase 1 (PSDR1): a new member				
RT	of the short-chain steroid dehydrogenase/reductase family highly				
RT	expressed in normal and neoplastic prostate epithelium."				
RT	Cancer Res. 61:1611-1618 (2001).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Liver;				
RA	Li K., Wang L., Cheng J., Zhang L., Lu Y., Liu Y., Duan H.,				
RT	"Screening of HCV core binding protein from human liver cDNA library				
RT	by using yeast two hybrid system."				
RT	Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.				
RP	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=20272150; PubMed=10810093;				
RA	Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.,				
RT	"Identification of novel human genes evolutionarily conserved in				
RT	Caenorhabditis elegans by comparative proteomics."				
RT	Genome Res. 10:703-713 (2000).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RC	TISSUE=Brain, Muscle, Placenta, and Prostate;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Browstein M.U., Usdin T.B., Toshiyuki S., Carrino C., Prange C.,				
RA	Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullany S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,				

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Halton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Maiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalls D.E.,
 RA Schenck A., Schein U.E., Jones S.J.M., Maria M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP IDENTIFICATION AS A RETINAL REDUCTASE, AND SUBCELLULAR LOCATION.
 RX MEDLINE-22151122; PubMed-12036956; DOI-10.1074/jbc.M202588200;
 RA Keshavilli N.Y., Chumakova O.V., Chetzkun S.V., Belyaeva O.V.,
 RA Lapshina E.A., Lin D.W., Matsumura M., Nelson P.S.,
 RT "Evidence that the human gene for prostate short-chain
 RT dehydrogenase/reductase (PSDR1) encodes a novel retinal reductase
 RT (RALR1).";
 RT J. Biol. Chem. 277:28909-28915(2002).
 CC -1- FUNCTION: Exhibits an oxidoreductive catalytic activity towards
 CC retinoids. Most efficient as an NADPH-dependent retinal reductase.
 CC Displays high activity toward 9-cis and all-trans-retinol. Also
 CC involved in the metabolism of short-chain aldehydes. No steroid
 CC dehydrogenase activity detected.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC Associated with endoplasmic reticulum membrane.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8TCL2-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8TCL2-2; Sequence=VSP_006159;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in the epithelial
 CC cells of prostate, in both basal and luminal secretory cell
 CC populations. Expressed at low levels in spleen, thymus, testis,
 CC ovary, small intestine, colon, peripheral blood leukocytes,
 CC kidney, adrenal gland and fetal liver. Not detected in prostatic
 CC fibromuscular stromal cells, endothelial cells, or infiltrating
 CC lymphocytes.
 CC -1- INDUCTION: By androgens, in prostate cancer cells.
 CC -1- PTM: Not glycosylated.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC -----
 DR EMBL: AF167438; AAF89632.1; -
 DR EMBL: AF935068; AAK72049.1; -
 DR EMBL: AF151840; AAD34077.1; -
 DR EMBL: BC000112; AAH00112.1; -
 DR EMBL: BC011727; AAH11727.1; -
 DR EMBL: BC026274; AAH26274.1; -
 DR EMBL: BC037302; AAH37302.1; -
 DR EMBL: BC051291; AAH51291.1; -
 DR HSSP: Q28960; INSD.
 DR GeneW: HGNC:17964; RDH11.
 DR MIM: 607849; -
 DR GO: GO:0005622; C:intracellular; ISS.
 DR GO: GO:0004745; P:retinol dehydrogenase activity; ISS.
 DR GO: GO:0045494; P:photoreceptor maintenance; ISS.
 DR GO: GO:0042572; P:retinol metabolism; ISS.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR002347; Adh_short_C2.
 DR Pfam: PF00106; adh_short_1.
 DR PRINTS: PR00081; GDHRD.
 DR PRINTS: PR00080; SDRFAMILY.

DR PROSITE, PS00061; ADH_SHORT; FALSE_NEG.
 KW Alternative splicing; Endoplasmic reticulum; NADP; Oxidoreductase;
 KM Signal-anchor; Transmembrane.
 FT TRANSMEM 1 21
 FT DOMAIN 22 318
 FT NP_BIND 48 54
 FT ACT_SITE 202 202
 FT VAASPIC 52 64
 FT CONFLICT 176 176
 FT CONFLICT 294 294
 FT CONFLICT 316 316
 SQ SEQUENCE 318 AA; 35386 MW; 5B0C36652774835 CRC64;
 Query Match 95.1%; Score 1577; DB 1; Length 318;
 Best Local Similarity 98.7%; Pred. No. 3,5e-120;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 1 MVELMPFLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGRVVTGANTGIGKETAKE 60
 1 MVELMPFLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGRVVTGANTGIGKETAKE 60
 61 LAQGARVYLACRDVEKELVAKELQTTGNQGVLRKLDSDTKSIRANAKGFAEKH 120
 61 LAQGARVYLACRDVEKELVAKELQTTGNQGVLRKLDSDTKSIRANAKGFAEKH 120
 121 LHWINNAGVMCPYSTADGPEMHGCVNHLGFLTLHLLETKSAPRIYNVSLAH 180
 121 LHWINNAGVMCPYSTADGPEMHGCVNHLGFLTLHLLETKSAPRIYNVSLAH 180
 121 LHWINNAGVMCPYSTADGPEMHGCVNHLGFLTLHLLETKSAPRIYNVSLAH 180
 181 HLGRHFNHNGEKFYVAGLAVCHSKLANILFQEDLARRLKSGVTVTSVHPPTVSELY 240
 181 HLGRHFNHNGEKFYVAGLAVCHSKLANILFQEDLARRLKSGVTVTSVHPPTVSELY 240
 241 RHSSFMKMMWMLSPFKITPQOGAOTRLHCALEGLSISGNHFSCHVAVSAQARNET 300
 241 RHSSFMKMMWMLSPFKITPQOGAOTRLHCALEGLSISGNHFSCHVAVSAQARNET 300
 301 IARRLMV 308
 301 IARRLMV 308
 301 IARRLMV 308
 RESULT 2
 CAG33461 PRELIMINARY; PRT; 318 AA.
 ID CAG33461
 AC CAG33461
 DT 01-JUN-2004 (TrEMBLrel. 27, Created)
 DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
 DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
 DE RDH11 protein.
 GN RDH11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RT "Cloning of human full open reading frames in Gateway(TM) system entry
 RT vector (pDONR201).";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR457180; CAG33461.1; -
 SQ SEQUENCE 318 AA; 35386 MW; 5B0C366552774835 CRC64;
 Query Match 95.1%; Score 1577; DB 2; Length 318;
 Best Local Similarity 98.7%; Pred. No. 3,5e-120;
 Matches 304; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 1 MVELMPFLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGRVVTGANTGIGKETAKE 60
 1 MVELMPFLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGRVVTGANTGIGKETAKE 60

QY 61 LA0GARVYIACRVEKGEIWAKEIOTTGNOQVYAKRLDSDPKSTRAMAKGFKAEK 120
 DB 61 LA0GARVYIACRVEKGEIWAKEIOTTGNOQVYAKRLDSDPKSTRAMAKGFKAEK 120
 QY 121 LHWIINNAGVWMCYSKTDADFEHNIQVNLHGFLLTHLLLEKLESAPSRIVVSSLAH 180
 DB 121 LHWIINNAGVWMCYSKTDADFEHNIQVNLHGFLLTHLLLEKLESAPSRIVVSSLAH 180
 QY 181 HLGSIIHHNLOGEFYNNAGLACYSKLANILFTDELARLKGSGVTTYSHGCTVQSELY 240
 DB 181 HLGSIIHHNLOGEFYNNAGLACYSKLANILFTDELARLKGSGVTTYSHGCTVQSELY 240
 QY 241 RHSSFMFMWMLFFSFFIKTPOGAQOTRLHCALTEGLEILSGNHFSDCHVAMVSAQARNET 300
 DB 241 RHSSFMFMWMLFFSFFIKTPOGAQOTRLHCALTEGLEILSGNHFSDCHVAMVSAQARNET 300
 QY 301 IARRLMDV 308
 DB 301 IARRLMDV 308
 QY 301 IARRLMDV 308
 DB 301 IARRLMDV 308
 RESULT 3
 RDHB_MOUSE
 ID RDHB_MOUSE STANDARD; PRT; 316 AA.
 AC Q9QYF1; Q9D0U5;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Retinol dehydrogenase 11 (EC 1.1.1.-) (Retinal reductase 1) (Rald1)
 DE (Prostate short-chain dehydrogenase/reductase 1) (Androgen-regulated
 DE short-chain dehydrogenase/reductase 1) (Short-chain aldehyde
 DE dehydrogenase) (SCALD) (Cell line WC/9.1L4 derived protein 1)
 DE (M2C60).
 DE Name=Rdh11; Synonym=Pedr1, Arsd1, Mdt1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Testis;
 RX MEDLINE=94289700; PubMed=8018917;
 RA Hara T., Harada N., Mitsui H., Wura T., Ishizaka T., Miyajima A.;
 RT "Characterization of cell phenotype by a novel cDNA library
 RT interleukin-4-dependent cell line.";
 RL Blood 84:189-199(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=2213316; PubMed=12137953; DOI=10.1016/S0378-1119(02)00718-7;
 RA Moore S., Pritchard C., Lin B., Ferguson C., Nelson P.S.;
 RT "Isolation and characterization of the murine prostate short-chain
 RT dehydrogenase/reductase 1 (Pedr1) gene, a new member of the short-
 RT chain steroid dehydrogenase/reductase family.";
 RL Gene 293:149-160(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22803395; PubMed=12807874; DOI=10.1074/jbc.M30496200;
 RA Kaasus-Jacobi A., Ou J., Bashmakov Y.K., Shelton J.M., Richardson J.A.,
 RA Goldstein J.L., Brown M.S.;
 RT "Characterization of mouse short-chain aldehyde reductase (SCALD), an
 RT enzyme regulated by steroid regulatory element-binding proteins.";
 RL J. Biol. Chem. 278:32380-32385(2003).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Niyazaki I., Otsu N., Saito K., Suzuki H., Yamanka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schirni L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusio V., Chohia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frerz K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson J.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongsava A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltase L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nunata K., Okido T., Pavan M.J., Pereira G.,
 RA Petrovsky N., Pillai R., Portius U.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sanderlin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carrinci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Waki J., Aizawa K., Aizawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shimagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Tsien T.B., Toshbnyk S., Carrinci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield J.S.N., Krzywinski M.I., Skalski U., Smalins D.E.,
 RA Scherch A., Schein J., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Exhibits an oxidoreductive catalytic activity towards
 CC retinoids. Most efficient as an NADPH-dependent all-trans-retinal
 CC reductase. Also involved in the metabolism of short-chain
 CC aldehydes.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC Associated with endoplasmic reticulum membrane (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced.
 CC Name=1;
 CC -!- TISSUE SPECIFICITY: Expressed at higher level in liver and testis.
 CC Expressed at lower levels in smooth muscle, thymus, submaxillary
 CC gland and epididymis. In testis, expression is restricted to
 CC pachytene spermatocytes. Also expressed in four layers of the
 CC retina, including the outer segment of rods and cones.
 CC -!- PTM: Not glycosylated (By similarity).
 CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to a
 CC frameshift in position 311.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC EMBL; AB035959; BAA8521.1; ALT_FRAME.
 CC EMBL; AY039032; AAK91516.1; -
 CC EMBL; AF474027; AAT79910.1; -
 CC EMBL; AK004413; BAB23296.1; -
 CC EMBL; BC018261; AAI18261.1; -
 CC HSSP; Q28960; INSD.
 CC MGD; MGI:102581; Rdh11.
 CC GO; GO:0005622; C:intracellular; ISS.
 CC GO; GO:0004745; F:retinol dehydrogenase activity; ISS.
 CC GO; GO:0045494; P:photoreceptor maintenance; ISS.
 CC GO; GO:0042572; P:retinol metabolism; ISS.
 CC InterPro; IPR002198; ADH_short.
 CC Pfam; PF00106; adh_short_C2.
 CC PRINTS; PR00081; GDRDH.
 CC PRINTS; PR00080; SDRFAMILY.
 CC PROSITE; PS00061; ADH_SHORT.
 CC KW Alternative splicing; Endoplasmic reticulum; NADP; Oxidoreductase; Signal-anchor; Transmembrane.
 CC TRANSMEM 1 21
 CC FT DOMAIN 22 316
 CC FT ACT_SITE 199 199
 CC FT NP_BIND 45 51
 CC FT CONFLICT 238 238
 CC FT CONFLICT 279 279
 CC SQ SEQUENCE 316 AA; 35148 MW; 62FAE25585CC05FE CRC64;

Query Match 81.2%; Score 1347.5; DB 1; Length 316;
 Best Local Similarity 84.3%; Pred. No. 1.8e-101;
 Matches 257; Conservative 20; Mismatches 27; Indels 1; Gaps 1;

QY 5 MFPLLLLL-LPFLLYMAAFOIRKMLSSGVCTSTVQLPGRVVVVTGANTGIGETAKELAQ 63
 DB 1 MFQFLLLSLPFLLYVTVPKIRKMLSSGVCTSNVQLPGKVAIVTGTANTIGETAKDLAQ 60
 QY 64 RGRVYLACADVKEKSELVAKEIOTTTGNOQVLRKLDSDPTKSIRAMKGFPAEKEHLV 123
 DB 61 RGRVYLACADVKEKSELVAKEIOTTTGNOQVLRKLDSDPTKSIRAMKGFPAEKEHLV 120
 QY 124 WINNAGVYMCPSYKTAADGFMHIGVNHGFLTLTHLLLEKESAPSRIVNSSLAHHLG 183
 DB 121 LINNAGVYMCPSYKTAADGFMHIGVNHGFLTLTHLLLEKESAPSRIVNSSLGHHLG 180
 QY 184 RIFHNHOGKRFYNAGLAVGSKLANTLFTQELARLKSGGVTVSVHGTQOSELVRS 243
 DB 181 RIFHNHOGKRFYSAGLAVGSKLANTLFTQELARLKSGGVTVSVHGTQOSELVRS 240
 QY 244 SFRMMWMLPSPFIKTPOQGAQTRLCALTEGLLEISGNHFSDDCHVAVWSAQAARNTIAR 303
 DB 241 SFRMMWMLPSPFIKTPOQGAQTRLCALTEGLLEISGNHFSDDCHVAVWSAQAARNTIAR 300
 QY 304 RLMDV 308
 DB 301 RLMDV 305

RESULT 4
 OQRI8 PRELIMINARY; PRT; 300 AA.
 AC OQRI8;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE UBE-1b;
 GN Name=Rdh11; Synonyms=Ube-1b;
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Testis;
 RA Goto M., Eddy E.M.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
 CC EMBL; AB030504; BAA82657.1; -
 CC MGD; MGI:102581; Rdh11.
 CC GO; GO:0016491; F:oxidoreductase activity; IEA.
 CC GO; GO:0008152; P:metabolism; IEA.
 CC InterPro; IPR002198; ADH_short.
 CC InterPro; IPR002347; Adh_short_C2.
 CC Pfam; PF00106; adh_short; 1.
 CC PRINTS; PR00081; GDRDH.
 CC PRINTS; PR00080; SDRFAMILY.
 CC KW Oxidoreductase.
 CC SEQUENCE 300 AA; 33240 MW; 7332230DB9057262 CRC64;

Query Match 77.8%; Score 1291; DB 2; Length 300;
 Best Local Similarity 85.6%; Pred. No. 6.7e-97;
 Matches 244; Conservative 18; Mismatches 23; Indels 0; Gaps 0;

QY 24 IRKMLSSGVCTSTVQLPGRVVVVTGANTGIGETAKELAQRGARVYLACADVKEKSELVAK 83
 DB 5 LRKMLSSGVCTSNVQLPGKVAIVTGTANTGIGETAKDLAQRGARVYLACADVKEKSELVAK 64
 QY 84 EIOTTTGNOQVLRKLDSDPTKSIRAMKGFPAEKEHLVWINNAGVYMCPSYKTAADGFE 143
 DB 65 EIQTAVTNSQVFPKAKDLADPTKSIRAPAKDFLAEKHLHLINNAGVYMCPSYKTAADGFE 124
 QY 144 MHIGVNHGFLTLTHLLLEKESAPSRIVNSSLAHHLGRIFHNHOGKRFYNAGLAVC 203
 DB 125 MHIGVNHGFLTLTHLLLEKESAPSRIVNSSLGHHLGRIFHNHOGKRFYSAGLAVC 184
 QY 204 HSKLANTLFTQELARLKSGGVTVSVHGTQOSELVRSFRRMMWMLPSPFIKTPOQ 263
 DB 185 HSKLANTLFTQELARLKSGGVTVSVHGTQOSELVRSFRRMMWMLPSPFIKTPOQ 244
 QY 264 AQTLYCALTEGLEISGNHFSDDCHVAVWSAQAARNTIARLMDV 308
 DB 245 AQTLYCALTEGLEISGNHFSDDCHVAVWSAQAARNTIARLMDV 289

RESULT 5
 OQRI9 PRELIMINARY; PRT; 293 AA.
 AC OQRI9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE UBE-1a;
 GN Name=Rdh11; Synonyms=Ube-1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Goto M., Eddy E.M.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
 CC EMBL; AB030503; BAA82656.1; -
 CC MGD; MGI:102581; Rdh11.
 CC GO; GO:0016491; F:oxidoreductase activity; IEA.
 CC GO; GO:0008152; P:metabolism; IEA.
 CC InterPro; IPR002198; ADH_short.
 CC InterPro; IPR002347; Adh_short_C2.
 CC Pfam; PF00106; adh_short; 1.

PRINTS; PRO0081; GDRDH.
DR PRINTS; PRO0080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 293 AA; 32442 MW; 1CAFFA9770F0E9D0 CRC64;

Query Match 77.1%; Score 1279; DB 2; Length 293;
Best Local Similarity 85.8%; Pred. No. 6.2e-96;
Matches 242; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY 27 MLSSGVCSTVQLGKVVVGTANTGIGKETAKELAGARVYLACRDVEKGEIVAKEIO 86
DB 1 MLSSGVCSTVQLGKVVVGTANTGIGKETAKELAGARVYLACRDVEKGEIVAKEIO 60
QY 87 TTTGNOQVLRKIDLSDTKSIKAMAKGPKAEKEKLHWNNAGVMMCPYSKTDGPEMHI 146
DB 61 AVTGNQGVYRKLDLADTKSIRAFKDFLAEEKHLHLINNAGVMMCPYSKTDGPEMHI 120
QY 147 GVNHLGHFLTLHLLEKLEKESAPRIYVNSSLAHHLGRIFHNLOGEKFFYNAGLAYCHSK 206
DB 121 GVNHLGHFLTLHLLEKLEKESAPRIYVNSSLAHHLGRIFHNLOGEKFFYNAGLAYCHSK 180
QY 207 LANILFTQELARLRKSGGVTTYSVHPGTVOSELVRRHSFMRMMWLFSFFIKTPQOGAQT 266
DB 181 LANILFTKELARLRKSGGVTTYSVHPGTVSELIRRSIMRMWLQFFFIKTPQOGAQT 240
QY 267 RLHICALTEGLEISGNHPSDCHVAVWSAQAARNETIARLMDV 308
DB 241 SLVLCALTEGLEISGSHFSDDQLAWVSQAAGNETIARLMDV 282

RESULT 6

Q6TUD3 PRELIMINARY; PRT; 407 AA.

AC Q6TUD3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE LRRGT00111.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Xu C.S., Chang C.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
RA Yang K.J., Zhao L.F., Ma H., Wang L., Wang S.F., Xing X.K., Shen G.M.,
RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.,
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
CC EMBL: AY387097; AAC91067.1; -
DR InterPro: IPR002198; Adh_short.
DR InterPro: IPR002347; Adh_short_C2.
DR Pfam: PF00106; adh_short_1.
DR PRINTS; PRO0081; GDRDH.
DR PRINTS; PRO0080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 407 AA; 44779 MW; FB0FA5B23D7BAC4 CRC64;

Query Match 75.9%; Score 1259.5; DB 2; Length 407;
Best Local Similarity 71.2%; Pred. No. 3.5e-94;
Matches 245; Conservative 25; Mismatches 33; Indels 41; Gaps 2;

QY 6 FPLLLLLPFL---LLYMAAPQIRKMLSSGVCSTVQLGKVVVGTANTGIGKETAKELA 62
DB 46 FCLLFLAYPLISSSTIYFLTPGSRKMLSCGVCTSNVQLSGKVAITGANTGIGKETAKDLA 105
QY 63 QR-----GARVYLACRDVEKGEIVAKE 84
DB 106 RRGKCTCSQLTSADVSP.LTVIWMVLPRLGIADWPFPRMFTGARVYLACRDVQKGEIVASE 165
QY 85 IOTTGNOQVLRKIDLSDTKSIKAMAKGPKAEKEKLHWNNAGVMMCPYSKTDGPEM 144

DB 166 IATTGNSQVLRKIDLADTKSIRAFAGFLAEKXYHLILINNAGVMMCPYSKTDGPEM 225

QY 145 HGVNHLGHFLTLHLLEKLEKESAPRIYVNSSLAHHLGRIFHNLOGEKFFYNAGLAYCH 204

DB 226 HGVNHLGHFLTLHLLEKLEKESAPRIYVNSSLAHHLGRIFHNLOGEKFFYNAGLAYCH 285

QY 205 SKLANILFTQELARLRKSGGVTTYSVHPGTVOSELVRRHSFMRMMWLFSFFIKTPQOGA 264

DB 286 SKLANILFTKELARLRKSGGVTTYSVHPGTVSELIRRSIMRMWLQFFFIKTPQOGA 345

QY 265 QTRICALTEGLEISGNHPSDCHVAVWSAQAARNETIARLMDV 308

DB 346 QSLVCAVTEGLEISGSHFSDDQLAWVSQAAGNETIARLMDV 389

RESULT 7

AAQ91067 PRELIMINARY; PRT; 407 AA.

AC AAQ91067;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE LRRGT00111.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Xu C.S., Chang C.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
RA Yang K.J., Zhao L.F., Ma H., Wang L., Wang S.F., Xing X.K., Shen G.M.,
RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.,
RL "Liver regeneration after PH."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY387097; AAQ91067.1; -
SQ SEQUENCE 407 AA; 44779 MW; FB0FA5B23D7BAC4 CRC64;

Query Match 75.9%; Score 1259.5; DB 2; Length 407;
Best Local Similarity 71.2%; Pred. No. 3.5e-94;
Matches 245; Conservative 25; Mismatches 33; Indels 41; Gaps 2;

QY 6 FPLLLLLPFL---LLYMAAPQIRKMLSSGVCSTVQLGKVVVGTANTGIGKETAKELA 62
DB 46 FCLLFLAYPLISSSTIYFLTPGSRKMLSCGVCTSNVQLSGKVAITGANTGIGKETAKDLA 105
QY 63 QR-----GARVYLACRDVEKGEIVAKE 84
DB 106 RRGKCTCSQLTSADVSP.LTVIWMVLPRLGIADWPFPRMFTGARVYLACRDVQKGEIVASE 165
QY 85 IOTTGNOQVLRKIDLSDTKSIKAMAKGPKAEKEKLHWNNAGVMMCPYSKTDGPEM 144
DB 166 IATTGNSQVLRKIDLADTKSIRAFAGFLAEKXYHLILINNAGVMMCPYSKTDGPEM 225
QY 145 HGVNHLGHFLTLHLLEKLEKESAPRIYVNSSLAHHLGRIFHNLOGEKFFYNAGLAYCH 204
DB 226 HGVNHLGHFLTLHLLEKLEKESAPRIYVNSSLAHHLGRIFHNLOGEKFFYNAGLAYCH 285
QY 205 SKLANILFTQELARLRKSGGVTTYSVHPGTVOSELVRRHSFMRMMWLFSFFIKTPQOGA 264
DB 286 SKLANILFTKELARLRKSGGVTTYSVHPGTVSELIRRSIMRMWLQFFFIKTPQOGA 345
QY 265 QTRICALTEGLEISGNHPSDCHVAVWSAQAARNETIARLMDV 308
DB 346 QSLVCAVTEGLEISGSHFSDDQLAWVSQAAGNETIARLMDV 389

RESULT 8

RDHC HUMAN
ID RDHC HUMAN STANDARD; PRT; 316 AA.
AC Q96NR8; O8TAM6;
DT 10-OCT-2003 (rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Retinol dehydrogenase 12 (EC 1.1.1.-).
GN Name=RDH12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RX [1]
RP SOURCE FROM N.A.
RC TISSUE=Cerebellum;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Setine M., Okeyashiki M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosotani T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Niinomura K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Houchi T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Imamura Y., Togiyama S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Inoue N., Watsanino K., Yuki H., Oshima A., Sasaki N., Aotaka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Teraishi Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishioaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kamagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujikawa T.,
RA Ono T., Yamada K., Fujii Y., Osaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hara H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegaki T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [12]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA DiCicco L., Matovina K., Farmer A.R., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Umed T.B., Toshikuni S., Carinini P., Prange C.,
RA Rana S.S., Loughran J.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S., McKean P.J., McKernan K.J., Malek J.A., Gunnarath P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madaen A., Rodrigues S., Sanchez A.,
RA Whitting M., Madaen A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywicki M.J., Skalska U., Smalios D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [13]
RP MEDLINE=22323226; PubMed=12226107; DOI=10.1074/jbc.M208862200;
RA Haeseler P., Yang G.-F., Iranishi Y., Driessen C.A.G.G.,
RA Matsunura M., Nelson P.S., Palczewski K.;
RT "Dial-substrate specificity short chain retinol dehydrogenases from

	RT	the vertebrate retina".
	RJ	J. Biol. Chem. 277:45537-45546(2002).
	CC	- FUNCTION: Exhibits an oxidoreductive catalytic activity towards
	CC	retinoids. Most efficient as an NADPH-dependent retinal reductase.
	CC	Displays high activity toward 9-cis and all-trans-retinol. Also
	CC	involved in the metabolism of short-chain aldehydes. No steroid
	CC	formation of 11-cis-retinal from 11-cis-retinol during
	CC	regeneration of the cone visual pigments.
	CC	- TISSUE SPECIFICITY: Widely expressed, mostly in eye, kidney,
	CC	brain, skeletal muscle and stomach.
	CC	- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
	CC	(SDR) family.
	CC	-- -- --
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	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
	CC	the European Bioinformatics Institute. There are no restrictions on its
	CC	use by non-profit institutions as long as its content is in no way
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	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
	CC	or send an email to license@sb.sib.ch).
	CC	-- -- --
	DR	EMBL; AK054835; BAB70811.1; -
	DR	EMBL; BC025724; AAH25724.1; -
	DR	HSSP; P140613; 1FDM.
	DR	Genew; HGNC:19977; RDH12.
	DR	GO; GO:0005622; C:intracellular; IDA.
	DR	GO; GO:0004745; F:retinol dehydrogenase activity; IDA.
	DR	GO; GO:0045494; P:photoreceptor maintenance; TAS.
	DR	GO; GO:0042572; P:retinol metabolism; IDA.
	DR	InterPro; IPR002347; Adh_short_C2.
	DR	Pfam; PF00106; adh_short; 1.
	DR	PRINTS; PR00081; GDRHDI.
	DR	PRINTS; PRO0080; SDRFAMILY.
	DR	PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
	KM	NADP; Oxidoreductase; Vision.
	FT	NP_BIND 46 52 NADP (by similarity).
	FT	ACT_SITE 200 200 By similarity.
	FT	CONFLICT 161 161 Q -> R (in Ref. 1).
	SQ	SEQUENCE 316 AA; 35065 MW; EX0B58CF93B67A8 CRC64;
		Query Match 68.1%; Score 1129; DB 1; Length 316;
		Best Local Similarity 71.2%; Pred. No. 1,1e-63;
		Matches 218; Conservative 34; Mismatches 52; Indels 2; Gaps 1;
QY	5	MPELLLLLPF-LIYMADPIRMKLSGVCSTVQLPGKVTVVTGANNGIGKEFAKELA 62
Db	1	MTVLTGLTLSPFSPLVMVAIPRIKKFFGGVCRINVOLPGKVVIITGANNGIGKETARELA 60
QY	63	ORGAGVYLACRPVEKGELVAKEIOTTTGNQOVLYRKLDSDPKSIAPAKAGFAEEKHLH 122
Db	61	SHGARVYLACRDVLKGSASAEIVDTKNISQVLYRKLDSDTKSIAPAFEGFLAEKQLH 120
QY	123	VWNNAGVWCPCYSKTADGFEMHIGNVHLGHFLTTHLLLEKTESAPSTIVNVSSLAHL 182
Db	121	IINNAGVWCPCYSKTADGFETHIGNVHLGHFLTITLLLEQLKVASAPAVNVSSVAHHI 180
QY	183	GRIHRHNIGKEFYTAGLAYCHGTLANILLTGCLARLKSGGVTTYSVHPGVQSEIVRH 242
Db	181	GRIPFHDLOESERYSRGPAVCHSLANVLTRELARKLOQTGVTIYAHPGVQSEIVRH 240
QY	243	SEFMAMMWLFEPFIKTQOQAQTRLCALTEGLEILISGNHPSDCIHAWAVNSAOAENETIA 302
Db	241	SELCLIMRLRPFPKTBREAQSLSHCALABGLEPLSGVTSDDCKRTVSPRAANNKTA 300
QY	303	IRLMVDY 308
Db	301	ERLMNV 306
		RESULT 9
		IDHC_BOVIN


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ID      RHMC BOVIN          STANDARD;          PRT;       316 AA.
DT      DT09837;
DT      10-OCT-2003 (Rel. 42, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      05-JUN-2004 (Rel. 44, Last annotation update)
DE      Retinol dehydrogenase 12 (EC 1.1.1.-) (Double substrate-specificity
DE      short chain dehydrogenase/reductase 2).
GN      Name=RDH12; Synonyms=DSSDR2;
OS      Bos taurus (bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC      Bovinae; Bos.
CX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Retina;
RX      MEDLINE=2232326; PubMed=12226107; DOI=10.1074/jbc.M208682200;
RA      Haeseleer F., Jiang G.-P., Imanishi Y., Driessen C.A.G.G.,
RT      Matsunura M., Nelson P.S., Palczewski K.;
RT      "Dual-substrate specificity short chain retinol dehydrogenases from
RL      the vertebrate retina.";
RL      J. Biol. Chem. 277:45537-45546(2002).
CC      -I- FUNCTION: Exhibits an oxidoreductive catalytic activity towards
CC      retinoids. Most efficient as an NADPH-dependent retinal reductase.
CC      Displays high activity toward 9-cis and all-trans-retinol. Also
CC      involved in the metabolism of short-chain aldehydes. No steroid
CC      formation detected. Might be the key enzyme in the
CC      formation of 11-cis-retinal from 11-cis-retinol during
CC      regeneration of the cone visual pigments (By similarity).
CC      -I- TISSUE SPECIFICITY: Expressed in the eyes.
CC      -I- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC      (SDR) family.
CC
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CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (see http://www.ebi.ac.uk/announcement/
CC      or send an email to license@ebi.ac.uk).
CC
CC      EMBL, AY115489; AAM51556.1; .
DR      GO; GO:0005622; C:intracellular; ISS.
DR      GO; GO:0004745; F:retinol dehydrogenase activity; ISS.
DR      GO; GO:0045494; P:photoreceptor maintenance; ISS.
DR      GO; GO:0042572; P:retinol metabolism; ISS.
DR      InterPro; IPRO02198; ADH_short.
DR      InterPro; IPRO02347; Adh_short_C2.
DR      Pfam; PF00106; adh_short; 1.
DR      PRINTS; PRO0081; GDRDH.
DR      PRINTS; PRO0080; SDRFAMILY.
DR      PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
KW      NADP; Oxidoreductase; Vision.
FT      ACT_SITE           46             52             NADP (by similarity).
FT      NP_BIND            200            By similarity.
SQ      SEQUENCE         316 AA; 35171 MW; 2582650B2CA04185 CRC64;
OY      Query Match              67.9%; Score 1126; DB 1; Length 316;
OY      Best Local Similarity    70.9%; Pred. NO. 2e-83;
OY      Matches 217; Conservative 36; Mismatches 51; Indels 2; Gaps 1;
DB      1 MLVVGILLTSPFLSYVAPSTIRKFRFAQGVCKRTDQLGKVAVITGANTIGKETARELA 60
DB      63 QRGARVYLACSDVEKGELVAKEIQTTNGOOVLVRKLDLSDTKSIRAWAKGFKAEEKIIA 122
DB      61 RRGARVVYIACBDVLGEASAASEIQADTKNSQVLVKLDLPSTKSIKRAPEAEFLAEKKQLH 120
OY      123 VWINNAGTMNCPYSTKADGPFEWHGWNLGHPLLTHILLEKIKESAPSRINVSIAHLH 182
OY      121 ILINNAGVMLCYSTKADGFFTHLVNHLGHLLPHLLLGRIKRSAPKRVNVLSVAHLH 180

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Cy		168	GRHFNHNLGKFKRYNAGLAVCSXKANILFQELARPKSGGWTTYSHPCTVSELYRH	242
Db		181	GKIRFPDLGDQKYXNLNGFAVCSSKIANYLPRELRKLAKGGVTYTAHPPIYANSKLVHR	240
Cy		243	SSPMRWMMWLFSEFFIKTPOCGAQTPLHALTEGLIEILSGNFSPDCHVAWWSAQARNETIA	3020
Db		241	SFLICLLMRLRFSFLTWTMGSAQTSLHCALLEGEPJLSGKFSDCKRTWVSFRANRXKA	3000
Cy		303	RRLMDV	308
Db		301	ERLMNV	306
RESULT 10				
RDHC_MOUSE				
ID	RDHC_MOUSE	STANDARD;	PRT;	316 AA.
AC	QBRYK; Q91WA5; Q9D1Y4;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DE	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Retinol dehydrogenase 12 (EC 1.1.1.-).			
CN	Name=rdh12;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RP	[1]			
SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=spinal cord;			
RX	MEBLINE=22354683; PubMed=1246651; DOI=10.1038/nature01266;			
RA	Okezaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotojiori T.,			
RA	Baldarelli R., Hill D.P., Salt C., Hume D.A., Quackenbush J.W.,			
RA	Schroll L.M., Kanapin D., Matsuda H., Batalov S., Beisel K.W.,			
RA	Blake U.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,			
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,			
RA	Gaasterland T., Gariboldi M., Giseli C., Goddix A., Gough J.,			
RA	Grimmond S., Gustinchich S., Hitokawa N., Jackson I.J., Jarvis E.D.,			
RA	Kanai A., Kawaji H., Kawasaki Y., Kedziarski R.M., King B.L.,			
RA	Konagaya A., Kurouchkin I.V., Lee Y., Lenhard B., Lyons P.A.,			
RA	Maglott D.R., Maltais L., Marchionni L., McKernie L., Miki H.,			
RA	Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,			
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,			
RA	Ravasi T., Reed U.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,			
RA	Sadelein A., Schneider C., Semple C.A., Setton M., Shmida K.,			
RA	Sultana R., Takemura Y., Taylor M.S., Teesdale R.D., Tomita M.,			
RA	Venardo R., Wagner L., Wahlstedt C., Wang Y., Warshawsky J., Wells C.,			
RA	Winning L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,			
RA	Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carrillo F., Hayatsu N.,			
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazutune N., Sato K.,			
RA	Shiratsuki T., Waki T., Kawai O., Atawa K., Arakawa T., Fukuda S.,			
RA	Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,			
RA	Myazaki A., Sakai K., Sasaki K., Shibata K., Shinagawa A.,			
RA	Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,			
RA	Binney E., Hayashizaki Y.,			
RT	"Analysis of the mouse transcritome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573(2002)."			
RN	[2]			
SEQUENCE FROM N.A.				
PC	TLSUB=Retina;			
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.24603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,			
RA	Altschuler S.F., Zeeberg B., Buacow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heselt F.,			
RA	Dischenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshlyuk S., Carinini P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bozak S.A., Mcwan P.O., McKernan K.J., Malek U.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,			

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Keltman A.C., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Exhibits an oxidoreductive catalytic activity towards
 CC retinoids. Most efficient as an NADPH-dependent retinal reductase.
 CC Displays high activity toward 9-cis and all-trans-retinol. Also
 CC involved in the metabolism of short-chain aldehydes. No steroid
 CC dehydrogenase activity detected. Might be the key enzyme in the
 CC formation of 11-cis-retinal from 11-cis-retinol during
 CC regeneration of the cone visual pigments (By similarity).
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC -----
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 CC -----
 DR EMBL: AK020927; BAB32258.1; -;
 DR EMBL: AK039233; BAC30288.1; -;
 DR EMBL: BC016204; AAL16204.1; -;
 DR HSSP: Q29860; 1NSD
 DR MGD; MGI:1926224; Rdn12.
 DR GO; GO:0005622; C:intracellular; ISS.
 DR GO; GO:0004745; P:retinol dehydrogenase activity; ISS.
 DR GO; GO:0045494; P:photoreceptor maintenance; ISS.
 DR GO; GO:0042572; P:retinol metabolism; ISS.
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR002347; Adh_short_C2.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00081; GDRDH.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
 KM NADP: Oxidoreductase; Vision.
 FT NP_BIND 46 52 NADP (By similarity).
 FT ACT_SITE 200 200 By similarity.
 FT CONFLICT 114 125 Missing (in Ref. 2).
 FT CONFLICT 120 120 H -> D (in Ref. 1; BAB32258).
 SQ SEQUENCE 316 AA; 35292 MW; CFS745BE710A6148 CRC64;
 Query Match 64.4%; Score 1068; DB 1; Length 316;
 Best Local Similarity 67.6%; Pred. No. 1,1e-78;
 Matches 207; Conservative 41; Mismatches 56; Indels 2; Gaps 1;
 QY 5 MFPELLLLLPFL-LYMAAPQIRKMLSSGVCTSTVQLPKRVVVTGANTGIGETAKELA 62
 DB 1 MFLIVLTLFSLILVLTAPSIKRFPAAGVCTTNVQIPGRVVITGANTGIGETARELA 60
 QY 63 ORGARVYLAQRDEKGEIVAKETIOTTGNOQVLYRKLDSPTKSTIRAMKGRKAEKHLH 122
 DB 61 RRGARVYLAQRDVLRKGSAASETRADKOSQVLRKLDSDTKSIAPFERFLAEIKHLH 120
 QY 123 VWINNAGVMCPYSKTADGEMHIGVNHGLHFLTLTLLEKLESAPSRIVVSSLAHHL 182
 DB 121 ILNINAGVMCPYSKTDGEPFEGVNHGLHFLTLTLLEKLESAPSRIVVSSLAHHL 180
 QY 183 GRHFNHLOGEKRYNAGLAYCHSKLANILFTQELARLRKSGVTTYVHPGVQSELYVH 242
 DB 181 GKIRFHLOQOKRYCSAFVAGHSKLANILFTRELARLRQGTGTAVAVHPGVVLSBITN 240
 QY 243 SSFRRMWMVLFSSFIKTPOGAGOTRLHCAITLGLTILSGNHFSDCVAVWSAQRNETIA 302
 DB 241 SYLLCLMLRLFSFPFSTSGCAQOTSLHCAIAEDLEFLSGKVFSDCKRMVVSRAARKYKA 300

QY 303 RRLMDV 308
 DB 301 ERLMNV 306
 RESULT 11
 Q6DG78
 ID Q6DG78 PRELIMINARY; PRT; 319 AA.
 AC Q6DG78;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 CC NCBI_TaxID=79551;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang U., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughelano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Keltman A.C., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RA and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Strausberg R.,
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC076473; AAL76473.1; -;
 KM Hypothetical protein.
 SQ SEQUENCE 319 AA; 34809 MW; 014DA5E135803B5A CRC64;
 Query Match 57.9%; Score 961; DB 2; Length 319;
 Best Local Similarity 63.3%; Pred. No. 5.7e-70;
 Matches 188; Conservative 44; Mismatches 65; Indels 0; Gaps 0;
 QY 12 LPELLYMAAPQIRKMLSSGVCTSTVQLPKRVVVTGANTGIGETAKELAIGARVYLA 71
 DB 13 LVAILILSLSPQIRKVAAGSCSSTVRLDQKVALVTGANGIGETAKELDILASGARVYLA 72
 QY 72 CRDVEKEVLAKETIOTTGNOQVLYRKLDSPTKSTIRAMKGRKAEKHLHWINNAGVM 131
 DB 73 CRDEKEAEAAAEIRTVGAKVEVRLDADCCSIRAFKQRLREVDDHILINNAGVM 132
 QY 132 MCPYSKTADGEMHIGVNHGLHFLTLTLLEKLESAPSRIVVSSLAHHLGRIFPHNLO 191
 DB 133 MCPYMKTRADGEMQIGVNHGLHFLTLTLGLKRSAPSRIVVSSLAHFGIRFPHDLH 192
 QY 192 GEKRYNAGLAYCHSKLANILFTQELARLRKSGVTTYVHPGVQSELYVHSSFFRRMWMV 251
 DB 193 SQGSYNGLAYCOSKLANILFTRELARLRKSGSVTVVAVHPGVRSBLVHSTLMSILFA 252
 QY 252 LFSFIKTPOGAGOTRLHCAITLGLTILSGNHFSDCVAVWSAQRNETIARLMDV 308

Db 253 FFSWFLSKSPKGAQTSICAVABELQISGKHFSDCAPAVAPQGRSEETARKLMVY 309

RESULT 12

Q9RLRS PRELIMINARY; PRT; 188 AA.
AC Q9RLRS; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE UBL-1c1.
GN Name=9430059D04R1k; Synonyms=Ube-1c;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Testis;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030505; BA82660.1; -
DR MGP; MGI:1915364; 9430059D04R1k.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002424; Insect adh_fam.
DR Pfam; PF00106; adh_short; 1-
DR PRINTS; PRO1167; INSAHFAMILY.
SQ SEQUENCE 188 AA; 21263 MW; BA54CC30F43098E7 CRC64;

Query Match 50.2%; Score 832; DB 2; Length 188;
Best Local Similarity 87.0%; Pred. No. 1e-59;
Matches 154; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 132 MCPSPKADGEMHIGVNHGHFLTHLLEKESPSRIYVNSLAHLLGRIHFENLQ 191
Db 1 MCPSPKADGEMHIGVNHGHFLTHLLEKESPSRIYVNSLAHLLGRIHFENLQ 60
QY 192 GERYNAGLAYCHSKLANILFTQELARRLKSGVTTYSVHGTVQSELVHSSFMKMMW 251
Db 61 GERYNAGLAYCHSKLANILFTQELARRLKSGVTTYSVHGTVQSELVHSSFMKMMW 120
QY 252 LFSFPIKTPQOAGQTRHCAITBGLILSGNHFSDCVAVNSAARNETIARRLMVY 308
Db 121 LFSFPIKTPQOAGQTRHCAITBGLILSGNHFSDCVAVNSAARNETIARRLMVY 177

RESULT 13

Q6DC71 PRELIMINARY; PRT; 291 AA.
AC Q6DC71; 01-OCT-2004 (TREMBlrel. 28, Created)
DT 01-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RL PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnate P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzyzinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC078208; AAH78208.1; -
KW Hypothetical protein.
SQ SEQUENCE 291 AA; 32141 MW; B7630F257D7C4386 CRC64;

Query Match 48.2%; Score 799.5; DB 2; Length 291;
Best Local Similarity 54.7%; Pred. No. 7.5e-57;
Matches 151; Conservative 54; Mismatches 70; Indels 1; Gaps 1;

QY 34 TSTVOLPKRVVVTGANTGIGETAKELAQGARVYLACRDVEKELVAKETQTTGNOQ 93
Db 6 SAAARDGKTVALITGANTGIGETAKELAQGARVYLACRDVEKELVAKETQTTGNOQ 65
QY 94 VLVRLDLSPTSTISAMAKGFAEKHLVWNNQVWCPSPKADGEMHIGVNHGH 153
Db 66 VVRLDLSPTSTISAMAKGFAEKHLVWNNQVWCPSPKADGEMHIGVNHGH 125
QY 154 FLTHLLEKLEKESAPSRIVNSLAHLLGRIHFENLQGERYVAGLAYCHSKLANILFT 213
Db 126 FLTHLLEKLEKESAPSRIVNSLAHLLGRIHFENLQGERYVAGLAYCHSKLANILFT 185
QY 214 QELARRLKSGVTTYSVHGTVQSELVHSSFMKMMWLFSPFKTPQOAGQTRHCAI 272
Db 186 QELARRLKSGVTTYSVHGTVQSELVHSSFMKMMWLFSPFKTPQOAGQTRHCAI 245
QY 273 TEGLEILSGNHFSDCVAVNSAARNETIARRLMVY 308
Db 246 DPALOTESGKYSDCAPAKAALNDDEVAQRLMEL 261

RESULT 14

Q6NV49 PRELIMINARY; PRT; 331 AA.
AC Q6NV49; 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE LOC407663 protein (Fragment).
GN Name=LOC407663;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RL MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Tissue=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 (SDR) family.
 DR EMBL: BC066739; AAH66739.1; -;
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR02347; Adh_short_C2.
 DR Pfam: PF0106; adh_short; 1.
 DR PRINTS: PR00081; GDRDH.
 DR PRINTS: PR00080; SDRFAMILY.
 DR Oxidoreductase.
 FT NON TER 1
 FT 1
 SQ SEQUENCE 331 AA; 37085 MW; 2AAAE0547EC4F CRC64;

Query Match 46.0%; Score 762.5; DB 2; Length 331;
 Best Local Similarity 51.7%; Pred. No. 9.1e-54;
 Matches 149; Conservative 57; Mismatches 79; Indels 3; Gaps 1;

QY 24 IRKMLSSGVCTSTVOLPGKVVVVGANTGIGKETAKELAORGARYVLAICRDEKGEVLVAK 83
 DB 36 LRRLAGVGRSKARLNGKTVLLTGNTGIGKETAYDMARKGARVILACDMSRAKAAE 95
 QY 84 EIOTTGNOQVLRKLDLSDTKSIRAMAKGFKAEKHLHWYINNAGVMMCPYKTDGFE 143
 DB 96 EIRKSGNENVTVMKDLASLGVRDLVKVQSQEQRDLILINNAGVMMCPKHTDEGFE 155
 QY 144 MHGVNHLGHFLTHLLLEKLSAPRIYVNSLAHLGRIFHNHLOGEKFNAGLAAC 203
 DB 156 MGIQVNLGHFLTLNLLDYLKKSAPRIYVNSVAHERKINFNINDKXDIPQSY 215
 QY 204 HSKLANILFTQELARLKSGVTTYSVHPTVQSELVRSSEFMKMMWL--FSFPIKTP 260
 DB 216 RSKLANVLFRELAIKLRDGTVTYALHPGVIRTELGRHVFSLMKRLILPFPFFKNP 275
 QY 261 QCGAQTRLHCAITGEGLEILSGNHFSDCHVAVSAQARNETIARLMDV 308
 DB 276 WQGAQTITTCVAVDESILKHSGLYSDCAPKETAPQGRDVAARLMDL 323

RESULT 15

AAH66739 PRELIMINARY; PRT; 331 AA.

AC AAH66739;
 DT 24-MAY-2004 (TrEMBLrel. 27, Created)
 DT 24-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DT 24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
 DE LOC007663 protein (Fragment).
 GN LOC007663
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22386257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derse J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marulava K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
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 RP SEQUENCE FROM N.A.
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 DR EMBL: BC066739; AAH66739.1; -;
 DR InterPro: IPR002198; ADH_short.
 DR InterPro: IPR02347; Adh_short_C2.
 DR Pfam: PF0106; adh_short; 1.
 DR PRINTS: PR00081; GDRDH.
 DR PRINTS: PR00080; SDRFAMILY.
 DR Oxidoreductase.
 FT NON TER 1
 FT 1
 SQ SEQUENCE 331 AA; 37085 MW; 2AAAE0547EC4F CRC64;

Query Match 46.0%; Score 762.5; DB 2; Length 331;
 Best Local Similarity 51.7%; Pred. No. 9.1e-54;
 Matches 149; Conservative 57; Mismatches 79; Indels 3; Gaps 1;

QY 24 IRKMLSSGVCTSTVOLPGKVVVVGANTGIGKETAKELAORGARYVLAICRDEKGEVLVAK 83
 DB 36 LRRLAGVGRSKARLNGKTVLLTGNTGIGKETAYDMARKGARVILACDMSRAKAAE 95
 QY 84 EIOTTGNOQVLRKLDLSDTKSIRAMAKGFKAEKHLHWYINNAGVMMCPYKTDGFE 143
 DB 96 EIRKSGNENVTVMKDLASLGVRDLVKVQSQEQRDLILINNAGVMMCPKHTDEGFE 155
 QY 144 MHGVNHLGHFLTHLLLEKLSAPRIYVNSLAHLGRIFHNHLOGEKFNAGLAAC 203
 DB 156 MGIQVNLGHFLTLNLLDYLKKSAPRIYVNSVAHERKINFNINDKXDIPQSY 215
 QY 204 HSKLANILFTQELARLKSGVTTYSVHPTVQSELVRSSEFMKMMWL--FSFPIKTP 260
 DB 216 RSKLANVLFRELAIKLRDGTVTYALHPGVIRTELGRHVFSLMKRLILPFPFFKNP 275
 QY 261 QCGAQTRLHCAITGEGLEILSGNHFSDCHVAVSAQARNETIARLMDV 308
 DB 276 WQGAQTITTCVAVDESILKHSGLYSDCAPKETAPQGRDVAARLMDL 323

Search completed: October 13, 2004, 18:13:07
 Job time : 77 secs